

Appl No. : 09/921,013
Filed : July 27, 2001

Cultures, which is associated with the Korea Research Institute of Bioscience and Biotechnology (hereafter "KRIBB"), an international depository authority, under accession (deposition) No. KCTC 0687BP on Nov. 3, 1999.

4. As part of their routine, scientists at KRIBB did a taxonomical study of the Species. The results of this study are attached as Appendix B (hereafter "the Study").

5. One part of the Study was a fatty acid analysis performed using the MIDI apparatus. The fatty acid analysis did not show a 100 % match with any known bacterial Species. Indeed, the analysis showed that the Species was only 47% like *Enterobacter sakazakii*. The best match according to this analysis was to *Pseudomonas agglomans*.

6. A second part of the Study compared the Species to the metabolic pathway diagnostics of other known bacteria. The first of these two panels of metabolic pathway diagnostics (API 20 NE) will identify gram-negative non-*Enterobacteriaceae* microorganisms. This first panel showed that the Species had a 93.6% identity with *Aerobacter hydrophylus*. The second of the two panels (API 20 E) identifies species and sub-species of *Enterobacteriaceae* as well as group and species identification of non-fermenting gram-negative bacteria. This second panel found that the Species had a 99.7% likeness with *Enterobacter sakazakii*. It is useful to note that the Species did not react the same way with four of the twenty individual tests that form the second panel. As the results indicate, 100% of the *sakazakii* bacteria react with the nitrate: reduction and oxidation (glucose) tests, while the Species did not react in either such test.

7. The Study also included a 16S ribosomal RNA analysis and comparison with other species. Based on this analysis, two phylogenetic trees were made to illustrate the relation between the Species and other bacteria that had the most similar RNA sequences. As can be seen on page 9 of the Study, the Species is not grouped together in a family with any other known bacteria.

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8. Finally, the Study sets forth on page 10 sets forth a carbon source utilization analysis ("Biolog") for the Species. This analysis is not compared to carbon source utilization analysis of other bacteria.

9. Based on the Study, KRIBB decided that the Species was a novel Species of *Enterobacter*. We named the Species *Enterobacter* sp. SSYL (KCTC 0687BP).

10. My co-inventor and I also subjected the Species to a comparative carbon source utilization test using the Biolog instrument and standard methods. We compared *Enterobacter sakazakii* with the Species and found that for the panel of 96 individual tests in the Biolog analysis, the two organisms gave the opposite results in 51 of the tests. Also, there was some question that the two organisms gave the same results in 20 of the other individual tests. (The read-out for this Biolog test is attached as Appendix C).

11. My co-inventors and I also did a comparative 16S ribosomal RNA analysis on the Species and on the *Enterobacter sakazakii* as wells as on the *Enterobacter cloacae* organisms. (The results of these two analyses are attached as Appendix D and E, respectively). The test showed that the Species had 98% identity with the *Enterobacter sakazakii* microorganism and 94.5% identity with *Enterobacter cloacae* microorganism.

12. The apparent closeness in the 16S ribosomal RNA analysis can be misleading when taken out of context of a full range of taxonomical testing. For instance, a BLAST search of the NCBI database (attached as Appendix F) shows that the in a similar analysis organisms from different genera such as *Citrobacter* (Page 6), *Salmonella* (Page 11) and *Klebsiella* (page 13) have a 97% identity reading with *Enterobacter sakazakii*. Thus, microorganisms can be clearly distinct from one another and have a misleadingly high percentage of identity. The Species is clearly different from either *Enterobacter sakazakii* or *Enterobacter cloacae* as confirmed by the above tests.

13. I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true, and further that

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these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Respectfully submitted,

Dated: May 26, 2003

By: 
Young Joo Kim

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Jeonmin-dong, Yuseong-gu,
Taejeon, Republic of Korea

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120402
S:\DOCS\PCSVCS-3007.DOC
052103



APPENDIX A

A list of Kim Y.J.'s representative publication

Publication

Kim YJ and Cramer SM, "Metal Affinity Displacement Chromatography of Proteins," *J. Chromatography* 549, 89-99 (1991).

Kim YJ, "Preparative Purification of Recombinant Thrombolytic Protein from Complex Biological Mixtures," *Biotechnology Techniques* 8(7), 457-462 (1994).

Kim YJ and Cramer SM, "Experimental Studies in Metal Affinity Displacement Chromatography of Proteins," *J. Chromatography A* 686, 193-203 (1994).

Hrushesky WJM, Langevin T, Kim YJ and Wood PA, "Circadian Dynamics of Tumor Necrosis Factor-alpha (Cachectin) Lethality," *J. Experimental Medicine* 180(3), 1059-1065 (1994).

Vunnum S, Gallant SR, Kim YJ and Cramer SM, "Immobilized Metal Affinity Chromatography: Modeling of Nonlinear Multicomponent Equilibrium," *Chemical Engineering Science* 50(11), 1785-1803 (1995).

Kim YJ, "SCX Separation of Recombinant Thrombolytic Protein from Complex Biological Feeds," *Biotechnology Techniques* 9(6), 417-422 (1995).

Kim SJ, Jang YC, Kil SG and Kim YJ, "Temperature Change Inside a Rubber Sheet During the Process of Heating and Cooling," *Polymer(Korea)* 19(2), 213-222 (1995).

Kim YJ, "Modeling of Non-Ideal Displacement Separation in Immobilized Metal Ion Affinity Chromatography," *Biotechnology Techniques* 9(9), 623-628 (1995).

Kim YJ, "Prediction of Protein Displacement by Simplified Immobilized Metal Ion Affinity Chromatographic Model," *Bioseparation* 5, 295-306 (1995).

Kim YJ, "Optimized Operating Parameters for the Displacement Separation of Biomolecules in Immobilized Metal Ion Affinity Chromatography," *Biotechnology Techniques* 13(12), 837-842 (1999).

Yang CS, Kim JS, Choi JW, Kwon MH, Kim YJ, Choi JG and Kim GT, "XPS Study of Aluminum Oxides Deposited on PET Thin Film," *Journal of Industrial and Engineering Chemistry* 6(3), 149-156 (2000).

Yang YL, Kim YJ, Kim KH and Oh E, "Separation of glycoprotein and its anticancer immunostimulating activity from dried barks of slippery Elm (*Ulmus parvifolia*)," *Korean J. Biotechnol. Bioeng.* 16(6), 547-553 (2001).

Yang YL and Kim YJ, "Immunostimulating exopolysaccharide with anticancer activity from *Enterobacter* sp. SSYL(KCTC 0687BP) screened from *Ulmus parvifolia*" *Korean J. Biotechnol. Bioeng.* 16(6), 554-561 (2001).

Books

Kim SJ, Kim JH and Kim YJ, "Unit Operations," *DongHwa KiSeul Publications*, ISBN 89-425-0502-3, pp 384, Korea, 1996.

Kim KY, No SY and Kim YJ, "New Combustion Engineering," *DongHwa KiSeul Publications*, ISBN 89-425-2404-4, pp 314, Korea, 1997.

Patents

Oh E, Kim YJ and Park HG, "Development of complex oral slow-release drug delivery system using alginate-polysaccharide beads", *Korea Patent* 245773 (Dec. 1, 1999), *Korea Patent* filing number 97-31780 (July 9, 1997).

Yang YL, Kim YJ, Kim KH and Oh E, "Peptido-glyco compounds separated from Slippery Elm for anticancer immunoactive material and the processes for the preparation of the material", *Korea Patent* 348870 (Aug. 1, 2002), *Korea Patent* filing number 2000-636 (Jan. 7, 2000).

Yang YL and Kim YJ, "Production of immunostimulating exopolysaccharide with anticancer activity from *Enterobacter* sp. SSYL (KCTC 0687BP) screened from *Ulmus parvifolia*," *Korea Patent* filing number 2000-43675 (July 28, 2000).

Yang YL and Kim YJ, "A Novel Microorganism Isolated from Chinese Elm (*Ulmus* Sp.) and Process for Preparing Exopolysaccharides by Employing the Microorganism," *US Patent* filing number 09/921,013 (July 27, 2001).

Kim YJ and Park KH, "Probe design methods for the detection of neighboring SNPs or nucleotide sequence mutations" *Korea Patent* filing number 2001-75283 (Nov. 30, 2001).

Kim YJ and Park KH, "Scoring and selection for optimum probes in probes design" *Korea Patent* filing number 2001-79722 (Dec. 15, 2001).

Kim YJ, Song MJ and Shim HS, "Method for detecting a defect in a microarray" *Korea Patent* filing number 2002-65521 (Oct. 25, 2002).

APPENDIX B

Fatty Acid Analysis Result Report

첨가물 1. 균체지방산 분석 결과 보고서

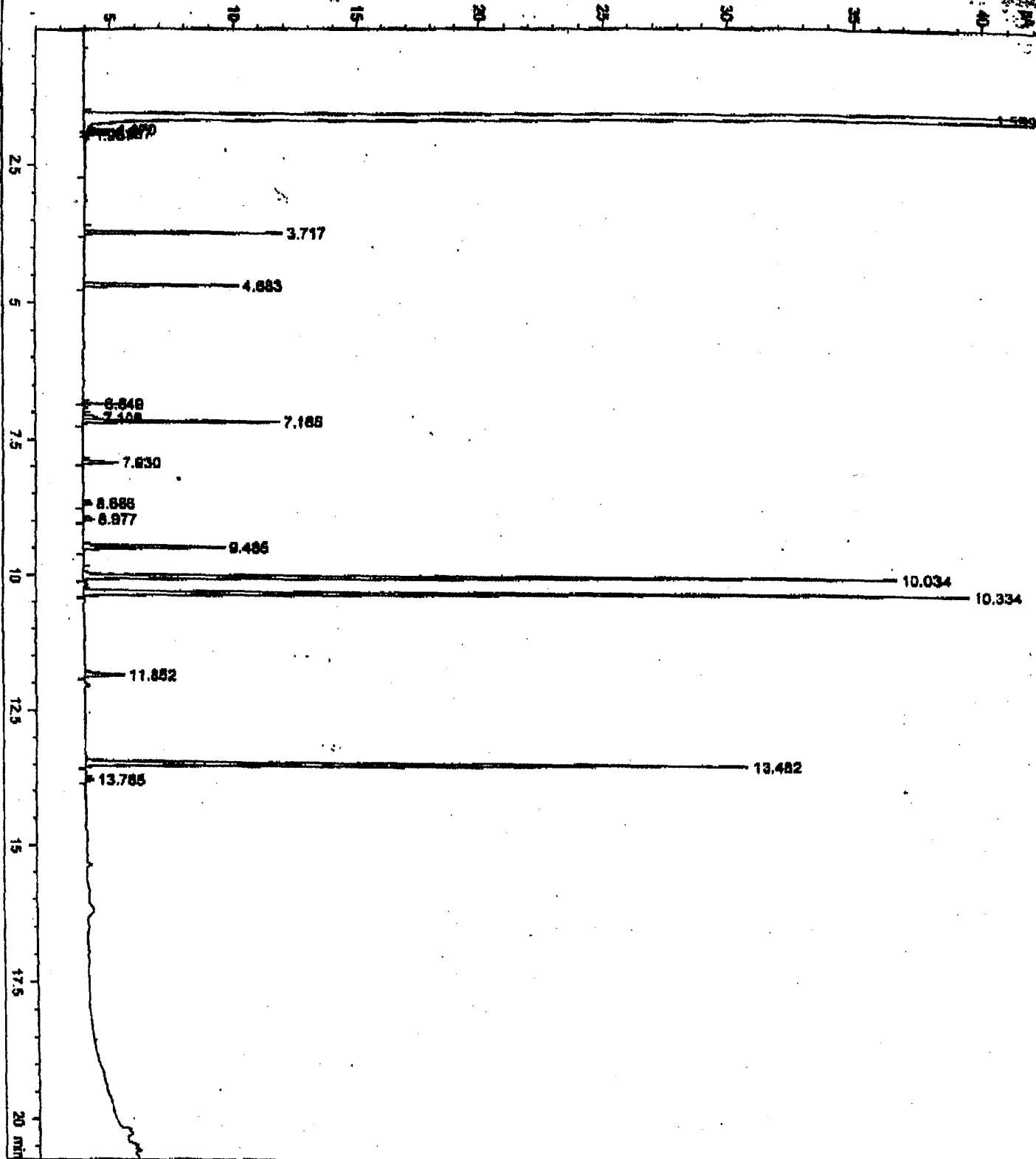
| 균주번호 | 접수번호 (BSID) |
|------|-------------|
| | 807-1, 2 |

● RESULTS

BSID-805-1, 2의 균체지방산 분석 결과를 첨부합니다. 의뢰균주는 MIDI 데이터 베이스의 균주들과 비교했을 때, Enterobacteriaceae family의 균주들과 가까운 것으로 분석되었습니다. API나 BIOLOG 결과와 비교하는 것이 좀 더 정확한 동정에 접근할 것으로 생각합니다.

1999년 1월 6일

균체지방산 분석 담당 이정숙/이근철



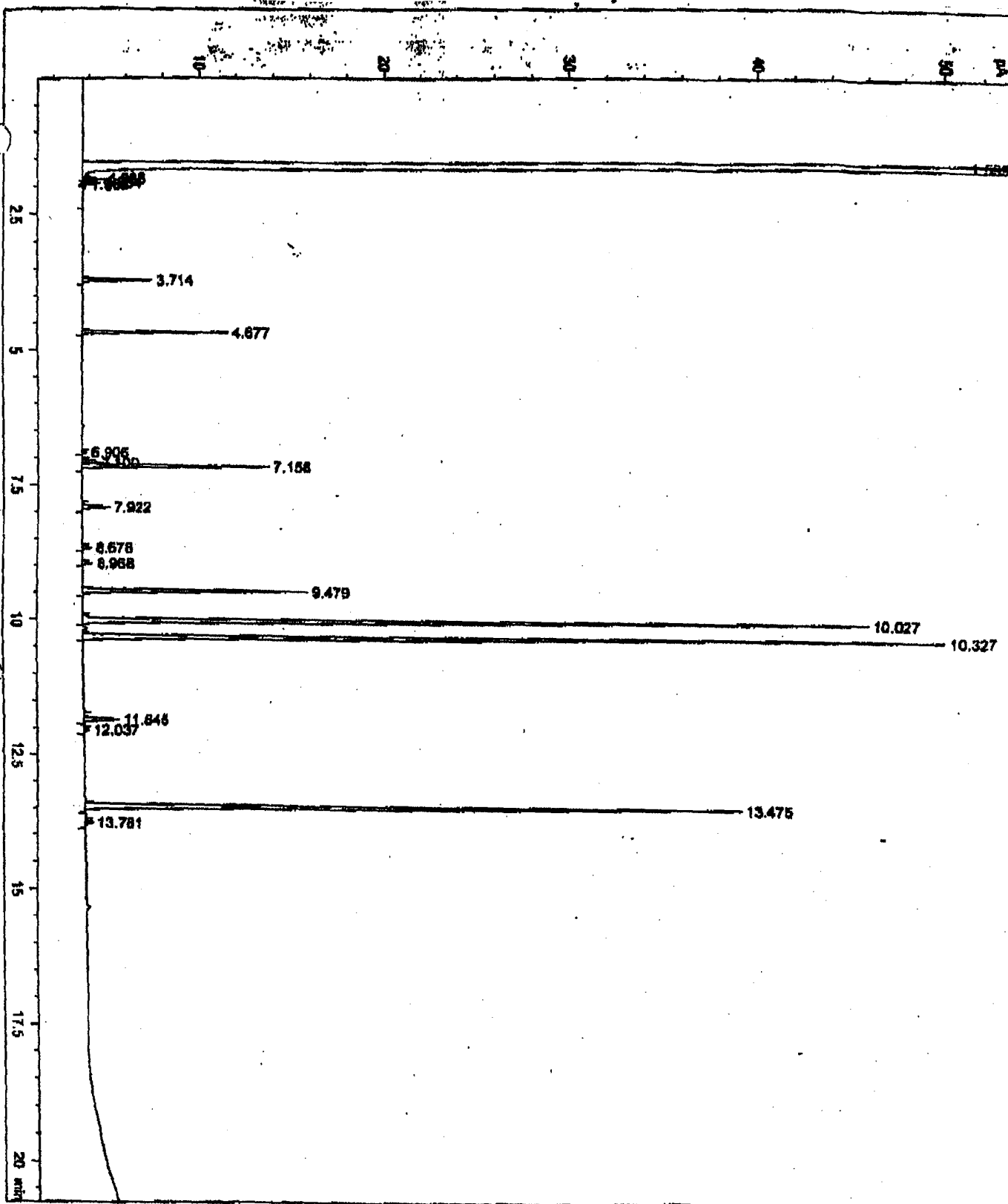
* * End f Rep rt ***

ID: 344 BSTD-807-1 (UNKNOWN) Date of run: 06-JUN-99 14:02:41
 Bottle: 12 SAMPLE

| RT | Area | Area/RT | Response | ECI | Name | Q | Comment 1 | Comment 2 |
|--------|-----------|---------|----------|--------|------------------|-------|---------------------|-----------------------|
| 1.889 | 435067406 | 0.027 | 7.008 | 7.008 | SOLVENT PEAK | | < min rt | |
| 1.878 | 3719 | 0.028 | 7.332 | 7.332 | | | < min rt | |
| 1.937 | 2474 | 0.021 | 7.506 | 7.506 | | | < min rt | |
| 1.967 | 343 | 0.018 | 7.747 | 7.747 | | | < min rt | |
| 3.717 | 28348 | 0.025 | 1.108 | 10.918 | Sum In Feature 3 | 4.58 | ECI deviates 0.004 | 12:0 ALDH ? |
| 4.693 | 22761 | 0.029 | 1.048 | 18.000 | 12:0 | 3.87 | ECI deviates 0.000 | Reference 0.009 |
| 6.648 | 528 | 0.008 | | 13.766 | | | < min area/rt | |
| 7.108 | 4289 | 0.042 | 0.878 | 13.857 | unknown 13.861 | 0.68 | ECI deviates -0.004 | |
| 7.148 | 35933 | 0.038 | 0.977 | 13.899 | 14:0 | 5.70 | ECI deviates -0.001 | Reference 0.007 |
| 7.930 | 6995 | 0.038 | 0.968 | 14.802 | unknown 14.803 | 1.10 | ECI deviates -0.001 | |
| 8.686 | 1944 | 0.040 | 0.988 | 15.000 | 15:0 | 0.30 | ECI deviates -0.000 | Reference 0.007 |
| 8.977 | 2891 | 0.039 | | 15.178 | | | | |
| 9.468 | 29827 | 0.040 | 0.948 | 15.486 | Sum In Feature 3 | 4.59 | ECI deviates 0.004 | 16:1 ISO I/14:0 30H |
| 10.034 | 171829 | 0.041 | 0.943 | 15.819 | Sum In Feature 4 | 26.33 | ECI deviates 0.002 | 16:1 w7a/15 iso 30H |
| 10.334 | 186332 | 0.041 | 0.941 | 16.001 | 16:0 | 28.48 | ECI deviates 0.001 | Reference 0.008 |
| 11.852 | 8971 | 0.042 | 0.933 | 16.888 | 17:0 CYCLO | 1.38 | ECI deviates 0.000 | Reference 0.006 |
| 13.482 | 180723 | 0.044 | 0.929 | 17.828 | Sum In Feature 7 | 22.74 | ECI deviates 0.001 | 18:1 w9a/w12t/w7a |
| 13.785 | 1880 | 0.046 | 0.928 | 17.999 | 18:0 | 0.38 | ECI deviates -0.001 | Reference 0.004 |
| ***** | 55175 | | | | SUMMED FEATURE 3 | 9.15 | 12:0 ALDH ? | unknown 10.828 |
| ***** | | | | | | | 16:1 ISO I/14:0 30H | 14:0 30H/16:1 ISO I |
| ***** | 171829 | | | | SUMMED FEATURE 4 | 26.33 | 16:1 w7a/15 iso 30H | 15:0 ISO 30H/16:1 w7c |
| ***** | 180723 | | | | SUMMED FEATURE 7 | 22.74 | 18:1 w7a/w8t/w12t | 18:1 w9a/w12t/w7a |
| ***** | | | | | | | 16:1 w12t/w8t/w7a | |

| Solvent Area | Total Area | Named Area | % Named | Total Area | Now Ref | ECI Deviation | Ref ECI Shift |
|--------------|------------|------------|---------|------------|---------|---------------|---------------|
| 435067406 | 648628 | 648612 | 99.57 | 615687 | 6 | 0.002 | 0.007 |

| | | | |
|-----------------------------|--|-------|---|
| TARA (Rev 3.90) Pantecan | | 0.893 | (Buth. agglomerans, Erwinia herbicola) |
| P. agglomerans | | 0.893 | (Buth. agglomerans, Erwinia herbicola) |
| P. ananas | | 0.807 | (Erwinia ananas) |
| Salmonella | | 0.737 | |
| S. typhimurium | | 0.737 | |
| S. C. CC subgroup A | | 0.737 | |
| S. typhi | | 0.507 | (confirm with other tests) |
| S. choleraesuis | | 0.448 | |
| S. S. choleraesuis | | 0.448 | |
| Enterobacter | | 0.704 | (excludes ATCC 35549 which is atypical) |
| E. cloacae | | 0.704 | (excludes ATCC 35549 which is atypical) |
| E. taylorae | | 0.694 | |
| E. sakazakii | | 0.448 | |
| CLIN (Rev 3.90) Citrobacter | | 0.564 | |
| C. diversus | | 0.564 | |
| C. amalonitius | | 0.287 | |
| Enterobacter | | 0.541 | |
| E. cloacae | | 0.541 | |
| E. C. CC subgroup A | | 0.541 | |
| Escherichia | | 0.516 | |
| E. hesnerii | | 0.516 | |
| E. coli subgroup B | | 0.291 | (high DNA homology with Shigella) |



* End of Report ***

PARACITAMOL

| Index | Area | Y | Z | Depth | ECI | Name | Comment 1 | Comment 2 |
|--------|----------|-------|-------|--------|------------------|------------|---------------------|-----------------------|
| 1.888 | 28884781 | 0.027 | | | 7.015 | BACKGROUND | < min rt | |
| 1.888 | 3718 | 0.028 | | | 7.888 | | < min rt | |
| 1.834 | 248D | 0.028 | | | 7.888 | | < min rt | |
| 1.848 | 384 | 0.019 | | | 7.780 | | < min rt | |
| 2.714 | 12418 | 0.026 | 1.080 | 10.820 | Sum In Feature 3 | 1.67 | ECI deviates 0.006 | 12:0 ALXN ? |
| 4.677 | 22918 | 0.025 | 1.038 | 12.000 | 12:0 | 3.71 | ECI deviates 0.000 | Reference 0.005 |
| 6.808 | 1148 | 0.028 | | 13.813 | | | | |
| 7.100 | 8086 | 0.023 | 0.978 | 13.957 | unknown 13.961 | 0.61 | ECI deviates -0.004 | |
| 7.186 | 4628D | 0.036 | 0.970 | 13.998 | 14:0 | 5.58 | ECI deviates -0.001 | Reference 0.005 |
| 7.922 | 7882 | 0.039 | 0.968 | 14.503 | unknown 14.503 | 0.90 | ECI deviates -0.000 | |
| 8.678 | 2380 | 0.040 | 0.960 | 18.000 | 18:0 | 0.28 | ECI deviates -0.000 | Reference 0.006 |
| 8.968 | 2601 | 0.038 | | 18.178 | | | | |
| 9.478 | 61946 | 0.040 | 0.984 | 18.484 | Sum In Feature 3 | 7.28 | ECI deviates 0.004 | 16:1 I80 I/14:0 30X |
| 10.027 | 226114 | 0.042 | 0.981 | 18.818 | Sum In Feature 4 | 26.53 | ECI deviates 0.002 | 16:1 w7a/15 I80 20X |
| 10.327 | 242544 | 0.041 | 0.948 | 16.001 | 16:0 | 28.41 | ECI deviates 0.001 | Reference 0.007 |
| 11.848 | 10723 | 0.044 | 0.943 | 16.888 | 17:0 CYCLO | 1.25 | ECI deviates -0.000 | Reference 0.005 |
| 12.037 | 1588 | 0.042 | 0.942 | 17.000 | 17:0 | 0.18 | ECI deviates 0.000 | Reference 0.005 |
| 13.478 | 201002 | 0.043 | 0.939 | 17.824 | Sum In Feature 7 | 23.30 | ECI deviates -0.001 | 18:1 w8a/w12a/w7a |
| 13.781 | 2381 | 0.043 | 0.938 | 18.000 | 18:0 | 8.27 | ECI deviates -0.000 | Reference 0.005 |
| ***** | 74188 | | | | STRONG FEATURE 3 | 8.96 | 12:0 ALXN ? | unknown 10.828 |
| ***** | | | | | | | 16:1 I80 I/14:0 30X | 14:0 30X/16:1 I80 I |
| ***** | 226114 | | | | STRONG FEATURE 4 | 26.53 | 16:1 w7a/15 I80 20X | 18:0 I80 20X/16:1 w7a |
| ***** | 201002 | | | | STRONG FEATURE 7 | 23.30 | 18:1 w7a/w8a/w12a | 18:1 w8a/w12a/w7a |
| ***** | | | | | | | 18:1 w12a/w8a/w7a | |

| Solvent Ar | Total Area | Masked Area | % Masked | Total Amt | Mask Amt | %CL Deviation | Mask %CL Shift |
|------------|------------|-------------|----------|-----------|----------|---------------|----------------|
| 438484471 | 852456 | 648907 | 99.56 | 810129 | 7 | -0.002 | -0.005 |

| | | | |
|-----------------|-----------------------------|-------|---|
| TARA [Rev 3.80] | <i>Vibrio</i> | 0.896 | (<i>Vib.</i> , agglomerans, <i>Erwinia herbicola</i>) |
| | <i>V. agglomerans</i> * | 0.894 | (<i>Vib.</i> , agglomerans, <i>Erwinia herbicola</i>) |
| | <i>V. anguillarum</i> ** | 0.507 | (<i>Erwinia anguilla</i>) |
| | <i>Salmonella</i> | 0.732 | |
| | <i>S. typhimurium</i> | 0.732 | |
| | <i>S. t.</i> QC subgroup A | 0.732 | |
| | <i>S. typhi</i> | 0.489 | (confirm with other tests) |
| | <i>S. choleraesuis</i> | 0.481 | |
| | <i>S. s. choleraesuis</i> | 0.481 | |
| | <i>Enterobacter</i> | 0.729 | (excludes ATCC 35549 which is atypical) |
| | <i>E. cloacae</i> * | 0.729 | (excludes ATCC 35549 which is atypical) |
| | <i>E. taylora</i> | 0.702 | |
| | <i>E. sakazakii</i> | 0.470 | |
| CIDM [Rev 3.80] | <i>Citrobacter</i> | 0.861 | |
| | <i>C. diversus</i> | 0.861 | |
| | <i>Enterobacter</i> | 0.815 | |
| | <i>E. cloacae</i> | 0.815 | |
| | <i>E. c.</i> QC subgroup A* | 0.815 | |
| | <i>Escherichia</i> | 0.809 | |
| | <i>E. hermannii</i> | 0.809 | |
| | <i>E. coli</i> subgroup E | 0.288 | (high DNA homology with <i>Shigella</i>) |

Refer no: 07NE

Date: 02/23/199

GOOD IDENTIFICATION

Strip : API 20 NE

V6.0

Read on: 02/23/199

Profile : 7 5 6 7 7 4 1

NO3 + TRP + GLU + ADH + URE - ESC + GEL - PNPG+ GLUa+ ARa+ MNEa+
MANa+ NAGa+ MALa+ GNTa+ CAPa- ADIa- MLTa+ CITa+ PACa- OX -

----- Significant taxa ----- % Id. --- T -- Tests against -----

Aer.hydro./caviae 93.6 0.33 3

Next choice

Chryseomonas luteola 6.2 0.19 3

POSSIBILITY OF *Vibrio fluvialis*

Aer.hydro./caviae : 3 test(s) against

GELATINE (HYDROLYSE) (GEL) 97 % CAPRATE (ASSIMILATION) (CAPa) 84
OXYDASE (OX) 99 %

Next choice

Chryseomonas luteola : 3 test(s) against

INDOLE (TRP) 0 % GLUCOSE (GLU) 13
N-ACETYL-GLUCOSAMINE (AS (NAGa) 12 %

COMPLEMENTARY TESTS :

GLUCOSEg 0/129 R
Aeromonas caviae : 2 % +
Vibrio fluvialis : 0 % -
Aeromonas hydrophila : 94 % +

Ref rence : 807E

Date : 02/23/195

DOUBTFUL PROFILE

Strip : API 20 E

V4.0

Read on: 02/23/195

Profile : 3 3 4 5 1 7 3 4 5

ONPG+ ADH + LDC - ODC + CIT + H2S - URE - TDA - IND + VP + GEL -
GLU + MAN + INO - SOR - RHA + SAC + MEL + AMY + ARA + OX - NO2 -
N2 - MOB + McC + OF/O- OF/F+

----- Significant taxa ----- % Id. --- T -- Tests against -----

Ent.sakazakii 99.7 0.18 4

Next choice
Ent.amnigenus 1 0.1 0.00 4

POSSIBILITY OF Enterobacter cloacae

Ent.sakazakii : 4 test(s) against

INDOLE (IND) 25 % myo-INOSITOL (INO) 75
NITRATE:REDUCTION EN NO(NO2) 100 % OXYDATION (GLUCOSE) (OF/O) 100

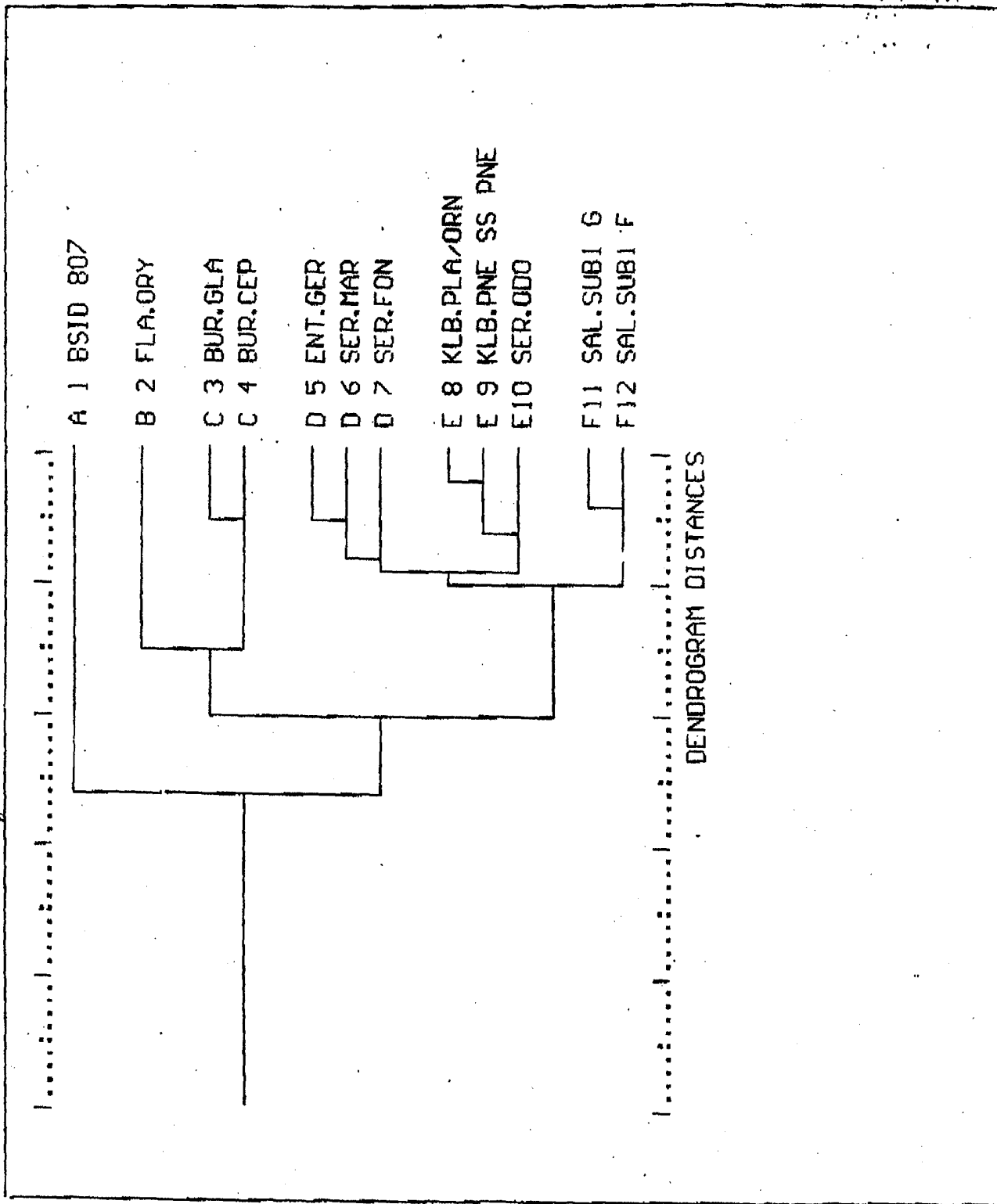
Next choice
Ent.amnigenus 1 : 4 test(s) against

ARGININE DIHYDROLASE (ADH) 25 % INDOLE (IND) 0
NITRATE:REDUCTION EN NO(NO2) 100 % OXYDATION (GLUCOSE) (OF/O) 100

COMPLEMENTARY TESTS :

Enterobacter cloacae : YELLOW ESC (HYD.) 30 %
Ent.sakazakii : 98 % 100 %

801) clinical Blood Chemistry



| water | α-cyclodextrin | dextrin | glycogen | tween 40 | tween 80 | N-acetyl-D-Galactosamine | N-acetyl-D-glucosamine | adonitol | L-arabinose | D-arabitol | cellulose |
|-----------------------------|----------------------|---------------------|----------------------|---------------------------|-------------------|--------------------------|------------------------|-------------------|--------------------------|------------------------|------------------------|
| - | - | + | + | - | - | + | + | + | + | + | - |
| D-erythritol | D-fructose | L-fructose | D-glucose | gentiobiose | α-D-glucose | m-inositol | α-D-lactose | lactulose | maltose | D-mannitol | D-mannose |
| - | - | + | + | + | - | + | + | + | + | + | + |
| D-melibiose | β-methyl D-glucoside | D-psicose | D-raffinose | L-rhamnose | D-sorbitol | sucrose | D-trehalose | lunrose | xylitol | sucetyl pyruvate | mono-sucetyl succinate |
| + | + | + | + | + | + | + | + | + | + | + | + |
| acetic acid | citric acid | citric acid | fumaric acid | D-galactonic acid lactone | D-galactonic acid | D-gluconic acid | D-glucosaminic acid | D-glucuronic acid | α-hydroxybutyric acid | β-hydroxybutyric acid | γ-hydroxybutyric acid |
| + | - | - | - | - | - | + | + | + | + | + | + |
| β-hydroxy phenylacetic acid | itaconic acid | α-keto butyric acid | α-keto glutaric acid | α-keto valeric acid | D,L-lactic acid | malonic acid | propionic acid | quinic acid | D-succinic acid | succinic acid | succinic acid |
| - | + | + | + | - | + | + | + | + | + | + | + |
| benzo succinic acid | succinamic acid | glucosaminid | alaninamide | D-alanine | L-alanine | L-alanyl-glycine | L-asparagine | L-aspartic acid | L-glutamic acid | glycyl-L-aspartic acid | glycyl-L-glutamic acid |
| + | + | + | + | + | + | + | + | + | + | + | + |
| L-Asidone | hydroxy L-proline | L-leucine | L-oronidine | L-phenylalanine | L-proline | L-pyroglutamic acid | D-serine | L-serine | L-threonine | D,L-carnitine | γ-amino butyric acid |
| + | + | + | + | + | + | + | + | + | + | + | + |
| thiostatic acid | inosine | uridine | thymidine | phenyl ethylamine | putrescine | 2-amino ethanol | 2,3-butanediol | glycerol | D,L-α-glycerol phosphate | glucose-1-phosphate | glucose-6-phosphate |
| + | + | + | + | + | + | + | + | + | + | + | - |

2 12/02/98 24 BSID 807 807 ? GN TSA/BUGM
BIO-NUMBER: 1 4 5 6 1 6 4 0 7 7 7 7 4 0 4 0 3 5 7 7 7 7 7 7 7 7 7 7 7 6

BEST ID: BURKHOLDERIA CEPACIA

BUR.CEP 0.003 24.085 1.375 3.713

BUR.GLA 0.003 24.337 0.750 4.963

SAL.SUB1 F 0.002 25.327 0.958 4.325

0.204 0.214 1.067 1.431 0.204 0.188 0.535 0.178 0.912 1.099 1.498 0.185
0.224 0.179 0.369 1.104 0.395 0.208 0.645 0.166 0.290 0.165 0.179 0.239
0.948 0.871 0.912 0.974 1.475 1.084 1.308 0.997 0.537 0.913 0.505 0.631
0.794 0.187 0.180 0.226 0.232 0.199 1.453 0.176 0.221 0.187 0.173 0.307
0.251 0.620 0.558 1.696 0.230 1.720 1.774 1.112 0.912 1.487 1.683 1.021
1.321 0.879 0.675 1.217 2.050 2.134 0.944 0.796 1.812 1.109 1.942 1.737
1.742 1.960 1.584 1.020 1.095 0.917 1.975 0.965 1.715 0.861 2.100 0.653
1.820 0.723 1.899 0.915 1.936 0.741 1.102 1.037 1.131 1.157 0.707 0.245

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 0 | 5 | 423 | 601 | 0 | -8 | 162 | -13 | 347 | 439 | 634 | -9 |
| 10 | -12 | 81 | 441 | 94 | 2 | 216 | -19 | 42 | -19 | -12 | 17 |
| 365 | 327 | 347 | 377 | 623 | 431 | 541 | 389 | 163 | 348 | 148 | 209 |
| 289 | -8 | -12 | 11 | 14 | -2 | 612 | -14 | 8 | -8 | -15 | 50 |
| 23 | 204 | 174 | 731 | 13 | 743 | 770 | 445 | 347 | 629 | 725 | 400 |
| 548 | 331 | 231 | 497 | 905 | 946 | 363 | 290 | 788 | 444 | 852 | 751 |
| 754 | 861 | 676 | 400 | 437 | 350 | 868 | 373 | 741 | 322 | 929 | 220 |
| 792 | 254 | 831 | 349 | 849 | 263 | 440 | 408 | 454 | 467 | 247 | 20 |

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[illegible]

APPENDIX C

첨부자료 3 : BIOLOG DATA

BIOLOG DATA

| water | α-cyclodextrin | dextrin | glycogen | tween40 | tween80 | N-acetyl-D-Galactosamine | N-acetyl-D-glucosamine | adonitol | L-arabinose | D-arabitol | cellobiose |
|-----------------------------|----------------------|---------------------|----------------------|---------------------------|---------------------|--------------------------|------------------------|-------------------|--------------------------|------------------------|------------------------|
| -(-) | -(-) | + | v(+) | v(-) | -(-) | v(+) | + | -(-) | + | -(-) | + |
| i-erythritol | D-fructose | L-fucose | D-galactose | gentiobiose | α-D-glucose | m-inositol | α-D-lactose | lactulose | maltose | D-mannitol | D-mannose |
| -(-) | + | v(+) | + | + | -(-) | -(-) | + | + | + | + | + |
| D-melibiose | β-methyl D-glucoside | D-psicose | D-raffinose | L-rhamnose | D-sorbitol | sucrose | D-trehalose | turanose | xylitol | methyl pyruvate | mono-methyl succinate |
| + | + | v(+) | + | v(+) | -(-) | + | + | + | -(-) | -(-) | -(-) |
| acetic acid | cis-aconitic acid | citric acid | formic acid | D-galactonic acid lactone | D-galacturonic acid | D-gluconic acid | D-glucosaminic acid | D-glucuronic acid | α-hydroxy butyric acid | β-hydroxy butyric acid | γ-hydroxy butyric acid |
| v(+) | + | + | v(-) | + | + | + | v(-) | + | -(-) | -(-) | -(-) |
| p-hydroxy phenylacetic acid | itaconic acid | α-keto butyric acid | α-keto glutaric acid | α-keto valeric acid | D,L-lactic acid | malonic acid | propionic acid | quinic acid | D-saccharic acid | sebacic acid | succinic acid |
| -(-) | -(-) | -(-) | -(-) | -(-) | v(+) | -(-) | -(-) | -(-) | -(-) | -(-) | v(+) |
| bromo succinic acid | succinamic acid | glucuronamide | alaninamide | D-alanine | L-alanine | L-alanyl-glycine | L-asparagine | L-aspartic acid | L-glutamic acid | glycyl-L-aspartic acid | glycyl-L-glutamic acid |
| -(-) | -(-) | v(+) | -(-) | -(-) | -(-) | v(+) | + | v(+) | -(-) | -(-) | -(-) |
| L-histidine | hydroxy L-proline | L-leucine | L-ornithine | L-phenyl alanine | L-proline | L-pyroglutamic acid | D-serine | L-serine | L-threonine | D,L-camitine | γ-amino butyric acid |
| -(-) | -(-) | -(-) | v(+) | -(-) | v(+) | -(-) | -(-) | + | -(-) | -(-) | -(-) |
| Urocanic acid | inosine | uridine | thymidine | phenyl ethylamine | putrescine | 2-amino ethanol | 2,3-butanediol | glycerol | D,L-α-glycerol phosphate | glucose-1-phosphate | glucose-6-phosphate |
| -(-) | + | v(+) | v(+) | -(-) | -(-) | -(-) | -(-) | + | v(+) | -(-) | -(-) |

Control: *Enterobacter sakazaki* () : Screened Cell

전기 BIOLOG DATA 는 인용문헌 1 에 개시된 균주 *Enterobacter sakazakii* 와 본원발명의 균주인 *Enterobacter sp.* SSYL(KCTC 0687BP)가 생존에 이용할 수 있는 물질을 측정하여 비교한 결과로서, ()의 내측에 기재된 결과는 본원발명의 균주를 대상으로 한 DATA 이고, ()의 외측에 기재된 결과는 인용문헌 1 에 개시된 균주를 대상으로 한 DATA 입니다. 전기 BIOLOG DATA 에서 보듯이, 본원발명의 균주와 인용문헌 1 에 개시된 균주는 테스트된 물질의 약 26% 정도에 대하여서만 동일한 결과를 나타내므로, 각 균주의 생존조건이 서로 상이함을 알 수 있습니다.

APPENDIX D

첨부자료 2: 인용문헌 1 의 균주에 대한 rRNA sequence 의 비교분석 자료

16S ribosomal RNA sequence data from *Enterobacter* sp. SSYL deposited under accession number KCTC 0687BP

ATTGAACGCTGGCGCAGGCCTAAACACATGCAAGTCGGGCGGTAGCACAGGAGCTTGCTCCCGGTGACGAGCGGGACGGGTGAGTAATGTCT
GGGAAACTGCTGATGAGGGGATAACTACTGGAACCGGTAGCTAATACCGCAIAACGTCTTCGGACCAAGTGCGGGACCTTCGGGCTCATGCC
ATCAGATGTGCCAGATGGGATTAGCTAGTAGGTGGGTAAAGGCTCACCTAGCGACGATCCCTAGTGTCTGAGAGGATGACCGCCACACT
GGAAGTGAACACCGTCCAGACTCTACGGGAGGCAGTGGGAATATTGCATGGCGCAAGCCTGATGCAGCCATGCCGCTGTATGAAG
AAGGCCTTCGGGTGTAAAGTACTTTACGCGAGGAGGAAGGTGTGTGGTTAATAACACAGCAATTGACGTTAATCGCAGAAAGACACCGGCTA
ACTCCGTGCCAGAGCCGCGGTAATACGGAGGTGCAAGCGTTAATCGGAATTACTGGCGTAAAGCGCACGCGGCTTGTAAAGTCAGATGT
GAAATCCCGGGCTCAACCTGGGAACCTGGAAGCTTGAAGCTGAGTCTGAGAGGGGTAGAATCCAGGTGTAGCGGTGAAATGCGT
AGAGATCTGGAGGAATACCGGTGGCAAGCGGCCCTGGACGAAGACTGACGCTCAGGTGCGAAAGCGTGGGAGCAACAGGATTAGATACC
CTGGTAGTCCACGCCGTAAACGATGTGCACTTGGAGGTTGTCCCTTGAGCGTGGCTTCCGAGCTAACCGGTTAAGTCGACCGCTGGGAGTAC
GGCGCAAGGTTAAACTCAATGAATTGACGGGGCCGACAAAGCGGTGGAGCACTCTGAGACAGGTGCTGCATGGCTGCTCAGTCAAGCAACCTTACCTGTT
CTTGACATCCAGAGAACTCTGCAGAGATGGGGAGTGCCCTTCGGGAACCTGAGACAGGTGAGTGGGAACCTCAAGGAGACTGCCGTGATAAACCGGAGGAA
GGTTAAGTCCCGCAACGAGCCCAACCTTATCTTTGTCGACGACGTAATGGTGGGAACCTCAAGGAGACTGCCGTGATAAACCGGAGGAA
GGTGGGATGACGTCAAGTCATCATGCCCCCTTACGACCGGCTACACACGTGCTACATGGCGCATACAAAGAGAGCTCTCGCGAGAGCAA
GCGGACCTCATAAAGTGGCTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGTAGTAATCGTAGATCAGAAATGCCACGGT
GAATACGTTCCCGGGCCTGTACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAGTAGTAGCTTAACCTTCGGGAGGGCGCTTACC
ACTTGTGATTCACTGGGGTG

<염기서열 상동성 조사 결과>

<http://www.ncbi.nlm.nih.gov>에서 Blast 를 사용하여 sequence homology 를 조사한 결과 *Enterobacter sakazakii* 균주와 98% homology 를 보이는 것으로 나타났다.

Enterobacter sakazakii gene for 16S ribosomal RNA, partial sequence Length = 1449

Score = 2617 bits (1320), Expect = 0.0
Identities = 1424/1453 (98%), Gaps = 8/1453 (0%)
Strand = Plus / Plus

KCTC 0687BP : 6 acgtggcggcaggcctaacacatgcaagtcggcggtagcacaggagc---ttgctcc 62
|||||
E. sakazakii: 1 acgtggcggcaggcctaacacatgcaagtcgaacggt---acaggagcagcttgctgc 58
|||||

KCTC 0687BP : 63 -cgggtgacgagcggcgacgggtgagtaatgtctgggaaactgccctgatggaggggat 121
| |
E. sakazakii: 59 tctgctgacgagtgccggacgggtgagtaatgtctgggaaactgccctgatggaggggat 118
| |

KCTC 0687BP : 122 aactactggaacggtagctaataccgcataaacgtcttcggaccacaaagtggggaccttc 181
|||||
E. sakazakii: 119 aactactggaacggtagctaataccgcataaacgtctacggaccacaaagtggggaccttc 178
|||||

KCTC 0687BP : 182 gggcctcatgccatcagatgtgcccagatgggattagctagtaggtgggtaaggctca 241
|||||
E. sakazakii: 179 gggcctcatgccatcagatgtgcccagatgggattagctagtaggtgggtaacggctca 238
|||||

KCTC 0687BP : 242 cctaggcgacgatccc tagctggtctgagaggatgaccagccacactggaactgagacac 301
|||||
E. sakazakii: 239 cctaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacac 298
|||||

KCTC 0687BP : 302 ggTccagactcctacggaggcagcagtgggaatatatgcacaaatggcgcaagcctgat 361
|||||
E. sakazakii: 299 ggTccagactcctacggaggcagcagtgggaatatatgcacaaatggcgcaagcctgat 358

KCTC 0687BP : 362 gcagccatgccgcgtgtatgaagaaggccttcgggttgtaaagtacittcagcgaggagg 421
|||||
E. sakazakii: 359 gcagccatgccgcgtgtatgaagaaggccttcgggttgtaaagtacittcagcgaggagg 418

KCTC 0687BP : 422 aaggtgttgtggttaataaccacagcaattgacgttactcgcagaagaagcaccggctaa 481
|||||
E. sakazakii: 419 aaggtgttgtggttaataaccgcagcaattgacgttaccgcagaagaagcaccggctaa 478

KCTC 0687BP : 482 ctccgtgccagcagccgcggttaatacggagggtgcaagcgttaatcggaattactggcg 541
|||||
E. sakazakii: 479 ctccgtgccagcagccgcggttaatacggagggtgcaagcgttaatcggaattactggcg 538

KCTC 0687BP : 542 taaagcgacgcaggcgggttgtttaagtcagatgtgaaatccccgggctcaacctgggaa 601
|||||
E. sakazakii: 539 taaagcgacgcaggcgggttgattaaagtcagatgtgaaatccccgggctcaacctgggaa 598

KCTC 0687BP : 602 ctgcatttgaaactggcaagcttgagctctgtagagggggtagaattccagggtgtagcg 661
 E. sakazakii: 599 ctgcatttgaaactggtcagcttgagctctgtagagggggtagaattccagggtgtagcg 658

KCTC 0687BP : 662 gtgaaatgcgtagagatctggaggaataccggtggcgaaggcgccccctggacgaagac 721
 E. sakazakii: 659 gtgaaatgcgtagagatctggaggaataccggtggcgaaggcgccccctggacgaagac 718

KCTC 0687BP : 722 tgacgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgc 781
 E. sakazakii: 719 tgacgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgc 778

KCTC 0687BP : 782 cgtaaacgatgtcgacttgaggttgtgcccttgaggcgtggcttcggagctaaccgct 841
 E. sakazakii: 779 cgtaaacgatgtcgacttgaggttgtgcccttgaggcgtggcttcggagctaaccgct 838

KCTC 0687BP : 842 taagtcgaccgcctggggagtagcgccgcaaggttaaactcaaatgaattgacgggggc 901
 E. sakazakii: 839 taagtcgaccgcctggggagtagcgccgcaaggttaaactcaaatgaattgacgggggc 898

KCTC 0687BP : 902 cgcacaagcgggtggagcatgtggtttaattogatcaacgcgaagaaccttacctggtc 961
|||||
E. sakazakii: 899 cgcacaagcgggtggagcatgtggtttaattogatcaacgcgaagaaccttacctggtc 958
|||||

KCTC 0687BP : 962 ttgacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtg 1021
|||||
E. sakazakii: 959 ttgacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtg 1018
|||||

KCTC 0687BP : 1022 ctgcatggctgtcgtcagctcgttgtgaaatgttgggttaagtcocgcaacgagcgca 1081
|||||
E. sakazakii: 1019 ctgcatggctgtcgtcagctcgttgtgaaatgttgggttaagtcocgcaacgagcgca 1078
|||||

KCTC 0687BP : 1082 acccttatacctttgttgcagcacgtaatggtgggaactcaaaggagactgccggtgata 1141
|||||
E. sakazakii: 1079 acccttatacctttgttgcagc-ggttcggccgggaactcaaaggagactgccggtgata 1137
|||||

KCTC 0687BP : 1142 aaccggaggaagtggggatgacgtcaagtcacatggcccttacgaccagggtacaca 1201
|||||
E. sakazakii: 1138 aaccggaggaagtggggatgacgtcaagtcacatggcccttacgaccagggtacaca 1197
|||||

KCTC 0687BP : 1202 cgtgctacaatggcgcatataaagagaagcgactctcgagagcaagcgacctcataa 1261
|||||
E. sakazakii: 1198 cgtgctacaatggcgcatataaagagaagcgac-ctcgagagcaagcgacctcataa 1256

KCTC 0687BP : 1262 agtgcgtcgtagtcggattggagctcgcaactcgactccatgaagtcggaatcgctagt 1321
|||||
E. sakazakii: 1257 agtgcgtcgtagtcggattggagctcgcaactcgactccatgaagtcggaatcgctagt 1316

KCTC 0687BP : 1322 aatcgtggtatcagaatgccacggtgaatacgttccgggacctgtacacacgcccggtca 1381
|||||
E. sakazakii: 1317 aatcgtggtatcagaatgccacggtgaatacgttccgggacctgtacacacgcccggtca 1376

KCTC 0687BP : 1382 caccatgggagtggttgcaaaagaagtaggtagcttaacctcgggagggcgcttacca 1441
|||||
E. sakazakii: 1377 caccatgggagtggttgcaaaagaagtaggtagcttaacctcgggagggcgcttacca 1436

KCTC 0687BP : 1442 ctttgtgattcat 1454
|||||
E. sakazakii: 1437 ctttgtgattcat 1449

APPENDIX E

첨부자료 4 : 인용문헌 2 의 균주에 대한 rRNA sequence 의 비교분석 자료

AF511434. *Enterobacter cloacae* [gi:21327114] from NCBI

16S ribosomal RNA sequence data of *Enterobacter cloacae* from NCBI

```

cctggcggca ggctaacac atgcaagtcg aacggtagca cagagagcct gctctgggtg gacgagtggc ggacgggtga gtaatgtctg ggaaactgcc tgatggaggg
ggataactac tggaaacggt agtaatacc gcataacgtc gcaagaccaa agagggggac cttcggcct cttgccatca gatgtgccca gatgggattia gctagtaggt
ggggtaacgg ctacacctagg cgacgatccc tagctggctc gagaggatga ccagccacac tggaaactgag acacgggtcca gactcctacg ggagggcagca gtggggaata
ttgcacaatg ggcgcaagcc tgaatcagcc atgccgcgtg tatgaagaag gcttcgggtg tgaagtac tticagcggg gaggaagggtg ttgtgggtta taaccgcagc aattgacgtt
accgcagaa gaagcacccg ctaactccgt gccagcagcc gcggtaatac ggagggtgca agcgttaatc ggaattactg ggcgtaaagc gcacgcaggc ggtctgtcaa
gtcggatgtg aaatcccccg gctcaacctg ggaactgcat tcgaaactgg caggctagag tctigttagag gggggtagaa ttccagggt agcgggtgaaa tgcgtagaga
tctggaggaa tacgggtggc gaaggcgcc ccttggacaa agactgacct tcagggtcca aagcgtgggg agcaaacagg attagatacc cttgtagtcc acgcogtaaa
cgatgtcgac ttggagggtg tgcctttag gcgtggcttc cggagctaac gcgttaagtc gaccgcctgg ggagtagcggc cgcaaggta aaactcaaat gaattgacgg
ggggccgcac aagcgggiga gcatgtggtt taattcgtg caacggaag aaccttaact actttgaca tccagagaac ttccagaga tggattggig ccttcgggaa ctctgagaca
ggigtgcat ggctgtctc agctcgtgtt gigaatgtt gggttaagtc ccgcaacccgt atccttgtt gccagcggc cggccgggaa ctcaaggag actgccagtg
ataaacigga ggaagggtggg gatgacgica agtcatcatg gcccttacg gtagggctac acacgtgcta caatggcgca tacaagaga agcgaactcg cgagagcaag
cggacctcat aaagtgcgtc gtagtcggga ttggagictg caactcgact ccatgaagtc ggaatcgta gtaatcgtag atcagaatgc tacgttcccg acgttcccg gcttgtaca
caccgcccgt cacaccaagg gagtgggtg caaagaagat aggtagctta accttcggga gggcgcttac cacttt

```

상기 검색된 *E. cloacae* 의 16S rRNA 유전자를 본원발명의 균주의 16S rRNA 와 비교한 결과는 다음과 같습니다.

scoring matrix: ,gap penalties: -12/-2

94.5% identity; Global alignment score: 5284

KCTC 0687BP : ATTGAACGCTGGCGGCGGCTAACACATGCAAGTCGGGCGGTAGCACAGGAGCTTGCT 60

E. cloacae : C-----CTGGCGGCGAGGCCTAACACATGCAAGTCGAACGGTAGCACAGAGCTTGCT 53

KCTC 0687BP : CCCGGGTGACGAGCGGCGGAGTGTCTGGGAACTGCCCTGATGGAGGGGGA 120

E. cloacae : CTCGGGTGACGAGTGGCGGACGGGTGAGTAATGTCTGGGAAACTGCCCTGATGGAGGGGGA 113

KCTC 0687BP : TAAC TACTGGAAACGGTAGCTAATACCGCATAACGTCTTCGGACCAAGTGGGGACCTT 180

E. cloacae : TAACTACTGGAAACGGTAGCTAATACCGCATAACGTGCGAAGACCAAGAGGGGACCTT 173

KCTC 0687BP : CGGGCCTCATGCCATCAGATGTGCCAGATGGGATTAGCTAGTAGGTGGGGTAAAGGCTC 240

E. cloacae : CGGGCCCTCTTGCCATCAGATGTGCCAGATGGGATTAGCTAGTAGGTGGGTAAACGGCTC 233

KCTC 0687BP : ACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCGACACTGGAAGAGACA 300

E. cloacae : ACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACA 293

KCTC 0687BP : CCGTCCAGACTCCTACGGGAGGCGAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGA 360

::

E. cloacae : CCGTCCAGACTCCTACGGGAGGCGAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGA 353

KCTC 0687BP : TGCAGCCATGCCGCGTGTATGAAGAAGGCCCTTCGGGTTGTAAAGTACTTTTCAGCGAGGAG 420

::

E. cloacae : TGCAGCCATGCCGCGTGTATGAAGAAGGCCCTTCGGGTTGTAAAGTACTTTTCAGCGGGGAG 413

KCTC 0687BP : GAAGGTGTTGTGTTAATAACCAACAGCAATTGACGTTACTCGCAGAAGAAGCACCGGCTA 480

::

E. cloacae : GAAGGTGTTGTGTTAATAACCGCAGCAATTGACGTTACCCGCAGAAGAAGCACCGGCTA 473

KCTC 0687BP : ACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGC 540

::

E. cloacae : ACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGGC 533

KCTC 0687BP : GTAAAGCGCACGCGGGTTTGTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGA 600

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E. cloacae : GTAAAGCGCACGCGGGTCTGTCAAGTCGGATGTGAAATCCCCGGGCTCAACCTGGGA 593

[illegible]

E. cloacae : ACTGCATTCCGAACTGGCAGGCTAGAGTCTTGTAGAGGGGGTAGAATCCAGGTGTAGC 653

KCTC 0687BP : GGTGAAATGCGTAGAGATCTGGAGGAATACCGTGGCGAAGGGCCCCCTGGACGAAGA 720
:::
:::

E. cloacae : GGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGCGCCCTTGGACAAAGA 713

KCTC 0687BP : CTGACGCTCAGGTGCGAAAGCGTGGGAGCAACAGGATTAGATACCCCTGGTAGTCCACG 780

E. cloacae : CTGACCTTCAGGTGCCAAGCGTGGGGAGCAACAGGATTAGATACCCCTGGTAGTCCACG 773

KCTC 0687BP : CCGTAAACGATGTCGACTTGGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAACGCG 840

E. cloacae : CCGTAAACGATGTCGACTTGAGGTTGTGCCCTTGAGGCGTGGCTTCCGGAGCTAAGCG 833

KCTC 0687BP : TTAAGTCGACCGCCTGGGGAGTACGGCCGCAAGTTAAAACTCAAATGAATTGACGGGGG 900

E. cloacae : TTAAGTCGACCGCCTGGGGAGTACGGCCGCAAGTTAAACTCAAATGAATTGACGGGGG 893

KCTC 0687BP : CCGCACAGCGGTGGAGCATGTGGTTAATTCGATGCAACGCGAAGACCTTACCTGGT 960

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E. cloacae : CCCGCACAAGCGGTGGAGCATGTGGTTAATTCGATGCAACGCGAAGAACCCTTACCTACT 953

KCTC 0687BP : CTTGACATCCAGAGAATCCTGCAGAGATGCGGGAGTGCCTTCGGGAACTCTGAGACACAGGT 1020
..... :
E. cloacae : CTTGACATCCAGAGAACTTCCAGAGATGGATTGGTGCCTTCGGGAACTCTGAGACACAGGT 1013

KCTC 0687BP : GGTGATGGCTGTCGTCAGCTCGTGTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGC 1080
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E. cloacae : GGTGATGGCTGTCGTCAGCTCGTGTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGC 1073

KCTC 0687BP : AACCTTATCCTTTGTTGCCAGCACGTAATGGTGGGAACTCAAAGGAGACTGCCCGGTGAT 1140
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E. cloacae : AACCTTATCCTTTGTTGCCAGCG-GTCCGGCCGGGAACTCAAAGGAGACTGCCAGTGAT 1133

KCTC 0687BP : AAACCGGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGACCAGGGCTACAC 1200
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KCTC 0687BP : ACGTGCTACAATGGCGCATACAAAGAGAGCGACTCTCGGAGAGCAAGCGGACCTCAT 1260

E. cloacae : ACGTGCTACAATGGCGCATACAAAGAGAACGAA-CTCGCGAGAGCAAGCGACCTCATA 1253

KCTC 0687BP : AAGTGCCTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAATCGCTAG 1320

E. cloacae : AAGTGGGTCGTAGTCCGGATTGGAGTCTGCAACTCGACTCCATGAAGTCGGAAATCGCTAG 1313

KCTC 0687BP : TAATCGTGGATCAGAAATGCCACGGTGAATACGTTCCCGGGCCTTGTACACACGCCCGTC 1380

E. cloacae : TAATCGTAGATCAGAAATGCTACGGTGAATACGTTCCCGGGCCTTGTAACACACCGCCGTC 1373

[illegible]

E. cloacae : ACACCATGGGAGTGGGTTGCAAGAAGTAGGTAGCTTAACCTTCGGGAGGGCGCTTACC 1433

KCTC 0687BP : ACTTTGTGATTCACTGGGGTG 1464

E. cloacae : ACTTT-----1436

**results of BLAST****BLASTN 2.2.6 [Apr-09-2003]****Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1051050953-025522-4328

Query=

(1449 letters)

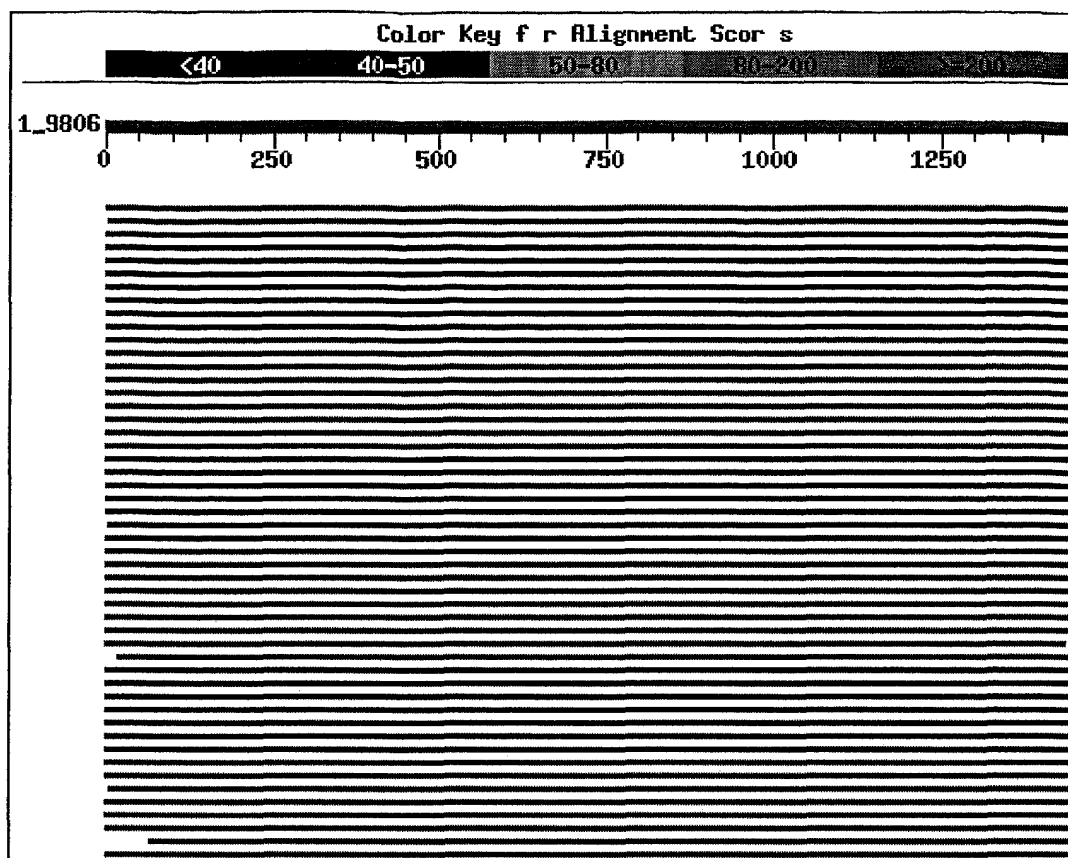
Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
1,729,678 sequences; 8,289,438,057 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)**Distribution of 100 Blast Hits on the Query Sequence**

Mouse-over to show defline and scores. Click to show alignments

APPENDIX F



| Sequences producing significant alignments: | | | | | Score (bits) | E Value |
|---|----------|-----|------------|---|-----------------|------------|
| gi | 2209038 | dbj | AB004746.1 | Enterobacter sakazakii gene for ... | 2872 | 0.0 |
| gi | 3169776 | gb | AF025366.1 | AF025366 Citrobacter diversus stra... | 2553 | 0.0 |
| gi | 16517821 | gb | AF423229.1 | Uncultured soil bacterium clone ... | 2549 | 0.0 |
| gi | 1857865 | gb | U88545.1 | STU88545 Salmonella typhi 16S riboso... | 2547 | 0.0 |
| gi | 2209047 | dbj | AB004755.1 | Klebsiella planticola gene for 1... | 2535 | 0.0 |
| gi | 18644561 | gb | AF371852.1 | Uncultured bacterium clone p-217... | 2522 | 0.0 |
| gi | 22758972 | gb | AF534193.1 | Uncultured bacterium clone Caf17... | 2516 | 0.0 |
| gi | 29468966 | gb | AY217654.1 | Escherichia senegalensis 16S rib... | 2492 | 0.0 |
| gi | 22758986 | gb | AF534207.1 | Uncultured bacterium clone Phe11... | 2492 | 0.0 |
| gi | 1899234 | gb | U90315.1 | SMU90315 Salmonella matopeni Sml 16S... | 2492 | 0.0 |
| gi | 1857864 | gb | U88548.1 | SPU88548 Salmonella paratyphi C 16S ... | 2492 | 0.0 |
| gi | 3169774 | gb | AF025364.1 | AF025364 Citrobacter sedlakii 16S ... | 2480 | 0.0 |
| gi | 2209040 | dbj | AB004748.1 | Enterobacter gergoviae gene for ... | 2478 | 0.0 |
| gi | 3169780 | gb | AF025370.1 | AF025370 Citrobacter amalonaticus ... | 2476 | 0.0 |
| gi | 6644288 | gb | AF208013.1 | AF208013 Enteric Group 137 16S rib... | 2472 | 0.0 |
| gi | 3169773 | gb | AF025363.1 | AF025363 Citrobacter rodentium 16S... | 2472 | 0.0 |
| gi | 4581981 | emb | AJ233408.1 | CFR233408 Citrobacter freundii 16... | 2468 | 0.0 |
| gi | 1916302 | gb | U92193.1 | SBU92193 Salmonella bovis morbifican... | 2468 | 0.0 |
| gi | 3169781 | gb | AF025371.1 | AF025371 Citrobacter farmeri 16S r... | 2466 | 0.0 |
| gi | 3169775 | gb | AF025365.1 | AF025365 Citrobacter freundii 16S ... | 2464 | 0.0 |
| gi | 20378116 | gb | AF373198.1 | Pantoea stewartii subsp. stewart... | 2460 | 0.0 |
| gi | 4581997 | emb | AJ233410.1 | EAM233410 Erwinia amylovora 16S r... | 2460 | 0.0 |
| gi | 3169779 | gb | AF025369.1 | Citrobacter sp. 'genomospecies 11... | 2460 | 0.0 |
| gi | 13873050 | gb | AF141895.1 | AF141895 Erwinia amylovora strain... | 2456 | 0.0 |

| | | | | | | | |
|----|----------|-----|------------|-----------|--------------------------------------|------|-----|
| gi | 3169783 | gb | AF025373.1 | AF025373 | Citrobacter werkmanii 16S... | 2454 | 0.0 |
| gi | 13873049 | gb | AF141894.1 | AF141894 | Erwinia amylovora strain... | 2452 | 0.0 |
| gi | 11907474 | emb | AJ277977.1 | LAD277977 | Leclercia adecarboxyla... | 2452 | 0.0 |
| gi | 3169778 | gb | AF025368.1 | AF025368 | Citrobacter braakii 16S r... | 2452 | 0.0 |
| gi | 4581973 | emb | AJ233403.1 | BGA233403 | Buttiauxella gaviniae 1... | 2448 | 0.0 |
| gi | 14549203 | dbj | AB053117.1 | | Klebsiella oxytoca gene for 16S... | 2448 | 0.0 |
| gi | 11907475 | emb | AJ277978.1 | LAD277978 | Leclercia adecarboxyla... | 2444 | 0.0 |
| gi | 2584810 | emb | Z96080.1 | PSZ96080 | Pantoea stewartii LMG 2715... | 2444 | 0.0 |
| gi | 3218459 | emb | X83265.1 | EA16SRR | E.amylovora 16S rRNA gene | 2444 | 0.0 |
| gi | 4753688 | emb | AJ010485.1 | EAM010485 | Erwinia amylovora 16S r... | 2444 | 0.0 |
| gi | 22947742 | gb | AY133084.1 | | Uncultured gamma proteobacterium... | 2440 | 0.0 |
| gi | 4582061 | emb | AJ233414.1 | EMA233414 | Erwinia mallotivora 16S... | 2436 | 0.0 |
| gi | 3282039 | emb | Y17667.1 | KOY17667 | Klebsiella oxytoca 16S rRN... | 2434 | 0.0 |
| gi | 2584741 | emb | Z96078.1 | ECZ96078 | Enterobacter cancerogenus ... | 2432 | 0.0 |
| gi | 1359900 | emb | X93216.1 | KP16SRRN2 | K.planticola 16S rRNA gen... | 2432 | 0.0 |
| gi | 22758992 | gb | AF534213.1 | | Uncultured bacterium clone Phe50... | 2428 | 0.0 |
| gi | 4581975 | emb | AJ233405.1 | BNO233405 | Buttiauxella noackiae 1... | 2422 | 0.0 |
| gi | 18419669 | gb | AF463533.1 | | Citrobacter sp. TSA-1 16S riboso... | 2420 | 0.0 |
| gi | 3282037 | emb | Y17663.1 | KPY17663 | Klebsiella planticola 16S ... | 2420 | 0.0 |
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| gi | 21436695 | emb | AJ489826.1 | UEN489826 | Enterobacteriaceae bac... | 2420 | 0.0 |
| gi | 2209046 | dbj | AB004754.1 | | Klebsiella oxytoca gene for 16S ... | 2418 | 0.0 |
| gi | 16417818 | gb | AF417870.1 | AF417870 | Pantoea sp. YSS/2001-2 1... | 2416 | 0.0 |
| gi | 3282054 | emb | Y17669.1 | KPY17669 | Klebsiella pneumoniae 16S ... | 2416 | 0.0 |
| gi | 6562390 | emb | AJ251468.1 | EAE251468 | Enterobacter aerogenes ... | 2416 | 0.0 |
| gi | 4581974 | emb | AJ233404.1 | BIZ233404 | Buttiauxella izardii 16... | 2415 | 0.0 |
| gi | 11557990 | emb | AJ293689.1 | BNO293689 | Buttiauxella noackiae ... | 2411 | 0.0 |
| gi | 10334693 | gb | AF181574.1 | AF181574 | Klebsiella planticola 16... | 2411 | 0.0 |
| gi | 27552380 | emb | AJ506794.2 | IBA506794 | Pantoea agglomerans 16... | 2409 | 0.0 |
| gi | 3282038 | emb | Y17666.1 | KOY17666 | Klebsiella ornithinolytica... | 2409 | 0.0 |
| gi | 3282036 | emb | Y17662.1 | KOY17662 | Klebsiella ornithinolytica... | 2409 | 0.0 |
| gi | 15088587 | gb | AF364844.1 | AF364844 | Pantoea ananatis strain ... | 2405 | 0.0 |
| gi | 3282032 | emb | Y17657.1 | KPY17657 | Klebsiella pneumoniae 16S ... | 2405 | 0.0 |
| gi | 4582002 | emb | AJ233413.1 | ECY233413 | Erwinia cypripedii 16S ... | 2405 | 0.0 |
| gi | 2570285 | gb | U80208.1 | ESU80208 | Erwinia stewartii 16S ribos... | 2403 | 0.0 |
| gi | 11557984 | emb | AJ293683.1 | BSP293683 | Buttiauxella sp. LBV 4... | 2403 | 0.0 |
| gi | 6562627 | emb | AJ251467.1 | KOR251467 | Klebsiella ornithinolyt... | 2401 | 0.0 |
| gi | 4581976 | emb | AJ233406.1 | BWA233406 | Buttiauxella warmboldia... | 2399 | 0.0 |
| gi | 11526813 | gb | AF221602.1 | AF221602 | Klebsiella sp. KGA 16S r... | 2397 | 0.0 |
| gi | 3282035 | emb | Y17661.1 | KOY17661 | Klebsiella oxytoca 16S rRN... | 2397 | 0.0 |
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| gi | 2570273 | gb | U80195.1 | EAU80195 | Erwinia amylovora 16S ribos... | 2397 | 0.0 |
| gi | 2209039 | dbj | AB004747.1 | | Enterobacter intermedius gene fo... | 2395 | 0.0 |
| gi | 22218216 | gb | AF529337.1 | | Uncultured gamma proteobacterium... | 2393 | 0.0 |
| gi | 4581972 | emb | AJ233402.1 | BFE233402 | Buttiauxella ferragutia... | 2393 | 0.0 |
| gi | 2209050 | dbj | AB004758.1 | | Pantoea ananas gene for 16S ribo... | 2393 | 0.0 |
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| gi | 15088588 | gb | AF364845.1 | AF364845 | Pantoea ananatis strain ... | 2389 | 0.0 |
| gi | 6693810 | gb | AF129444.1 | AF129444 | Klebsiella trevisanii str... | 2389 | 0.0 |
| gi | 6693809 | gb | AF129443.1 | AF129443 | Klebsiella planticola str... | 2389 | 0.0 |
| gi | 3282052 | emb | Y17658.1 | KTY17658 | Klebsiella terrigena 16S r... | 2389 | 0.0 |
| gi | 29468325 | gb | AF494202.1 | | Serratia marcescens strain N9 16... | 2387 | 0.0 |
| gi | 11526814 | gb | AF221603.1 | AF221603 | Klebsiella sp. KG1 16S r... | 2387 | 0.0 |
| gi | 2584740 | emb | Z96088.1 | EAZ96088 | Erwinia amylovora LMG 2024... | 2387 | 0.0 |
| gi | 1240062 | emb | X80678.1 | SS16SRDNG | S.shomron 16S rRNA gene | 2387 | 0.0 |
| gi | 12044275 | gb | AF310218.1 | AF310218 | Kluyvera cryocrescens 16... | 2383 | 0.0 |
| gi | 11557988 | emb | AJ293687.1 | BNO293687 | Buttiauxella noackiae ... | 2383 | 0.0 |
| gi | 2209048 | dbj | AB004756.1 | | Klebsiella ornithinolytica gene ... | 2383 | 0.0 |
| gi | 26225097 | gb | AY167970.1 | | Swine manure bacterium 37-11 16S... | 2381 | 0.0 |

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| gi 15027281 emb AJ318112.1 UGA318112 | Uncultured gamma prote... | 2381 | 0.0 |
| gi 4205080 gb U78182.1 KOU78182 | Klebsiella ornithinolytica ... | 2381 | 0.0 |
| gi 22218235 gb AF529356.1 | Uncultured gamma proteobacterium... | 2379 | 0.0 |
| gi 23955492 gb AF543283.1 | Klebsiella oxytoca strain ChDC O... | 2377 | 0.0 |
| gi 19908366 gb AY082447.1 | Enterobacter sp. 253a 16S riboso... | 2377 | 0.0 |
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| gi 3282055 emb Y17670.1 KTY17670 | Klebsiella terrigena 16S r... | 2373 | 0.0 |
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| gi 3309664 gb AF076154.1 AF076154 | Erwinia cypripedii 16S ri... | 2371 | 0.0 |
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| gi 6714906 gb AF130981.1 AF130981 | Klebsiella pneumoniae 16S... | 2365 | 0.0 |

Alignments

Get selected sequences

Select all

Deselect all

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Strand = Plus / Plus

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Score = 2553 bits (1288), Expect = 0.0
 Identities = 1405/1445 (97%)
 Strand = Plus / Plus

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4/22/03

Sbjct: 860 gaccgcctggggagtagcgccgcaagggttaaaactcaaattgacgggggcccgcac 919

Query: 905 aagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctgggtcttgaca 964
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Sbjct: 920 aagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctgggtcttgaca 979

Query: 965 tccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgctgcat 1024
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Sbjct: 980 tccacagaagttktcagagatgagmatgtgccttcgggaaccgtgagacaggtgctgcat 1039

Query: 1025 ggctgtcgtcagctcgtgtgtgaaatgttgggttaagtcccgcaacgagcgcaaccctt 1084
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Sbjct: 1040 ggctgtcgtcagctcgtgtgtgaaatgttgggttaagtcccgcaacgagcgcaaccctt 1099

Query: 1085 atcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaacggga 1144
 |||||

Sbjct: 1100 atcctttgttgccagcggttcggccgggaactcaaaggagactgccagtgataaactgga 1159

Query: 1145 ggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgtgcta 1204
 |||||

Sbjct: 1160 ggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgtgcta 1219

Query: 1205 caatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtgcgtc 1264
 |||||

Sbjct: 1220 caatggcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtatgtc 1279

Query: 1265 gtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaaatcgtagg 1324
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Sbjct: 1280 gtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaaatcgtagg 1339

Query: 1325 atcagaatgccacggtgaatacgttccccgggccttgtagacacaccgcccgtcacaccatgg 1384
 |||||

Sbjct: 1340 atcagaatgccacggtgaatacgttccccgggccttgtagacacaccgcccgtcacaccatgg 1399

Query: 1385 gagtgggttgcaaaaagaagtaggttagcttaaccttcgggagggcgcttaccactttgtga 1444
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Sbjct: 1400 gagtgggttgcaaaaagaagtaggttagcttaaccttcgggagggcgcttaccactttgtga 1459

Query: 1445 ttcac 1449
 |||||

Sbjct: 1460 ttcac 1464

>gi|16517821|gb|AF423229.1| Uncultured soil bacterium clone 144-1 16S ribosomal
 sequence
 Length = 1465

Score = 2549 bits (1286), Expect = 0.0
 Identities = 1410/1450 (97%), Gaps = 1/1450 (0%)

Strand = Plus / Plus

```

Query: 1      acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
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Sbjct: 6      acgctggcggcaggcctaacacatgcaagtcgaacggtaacaggaagcagcttgctgctt 65

Query: 61     tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
              |||||||
Sbjct: 66     tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 125

Query: 121    ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180
              |||||||
Sbjct: 126    ctactggaaacggtagctaataccgcataacgtcgcaagaccaaagagggggaccttcgg 185

Query: 181    gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
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Sbjct: 186    gcctcttgccatcggatgtgcccagatgggattagctagtaggtggggtaacggctcacc 245

Query: 241    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
              |||||||
Sbjct: 246    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 305

Query: 301    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
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Sbjct: 306    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 365

Query: 361    agccatgccgcgtgtatgaagaaggccttcggggtgttaaagtactttcagcggggaggaa 420
              |||||||
Sbjct: 366    agccatgccgcgtgtatgaagaaggccttcggggtgttaaagtactttcagcggggaggaa 425

Query: 421    ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
              |||||||
Sbjct: 426    ggtgttgaggttaataacctcagcaattgacgttaccgcgagaagaagcaccggctaact 485

Query: 481    ccgtgccagcagccgcggttaatacggaggggtgcaagcg-ttaatcggaattactgggcgt 539
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Sbjct: 486    ccgtgccagcagccgcggttaatacggaggggtgcaagcgggttaatcggaattactgggcgt 545

Query: 540    aaagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaac 599
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Sbjct: 546    aaagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaac 605

Query: 600    tgcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 659
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Query: 660    tgaaatgcgtagagatctggaggaataccgggtggcgaaggcggccccctggacgaagact 719
              |||||||

```

Sbjct: 666 tgaaatgcgtagagatctggaggaataaccggtggcgaaggcggccccctggacaaagact 725

Query: 720 gacgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgcc 779
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Sbjct: 726 gacgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgcc 785

Query: 780 gtaaacgatgtcgacttggaggttgtgcccttgaggcgtggcttccggagctaacgcgtt 839
|||||

Sbjct: 786 gtaaacgatgtcgacttggaggttgtgcccttgaggcgtggcttccggagctaacgcgtt 845

Query: 840 aagtcgaccgcctggggagtagcggccgcaagggttaaaactcaaataaattgacggggggcc 899
|||||

Sbjct: 846 aagtcgaccgcctggggagtagcggccgcaagggttaaaactcaaataaattgacggggggcc 905

Query: 900 cgcacaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtct 959
|||||

Sbjct: 906 cgcacaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactct 965

Query: 960 tgacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgc 1019
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Sbjct: 966 tgacatccagagaacttagcagagatgctttggtgccttcgggaactctgagacaggtgc 1025

Query: 1020 tgcattggctgtcgtcagctcgtgttgtaaagtgttggttaagtcccgcaacgagcgcaa 1079
|||||

Sbjct: 1026 tgcattggctgtcgtcagctcgtgttgtaaagtgttggttaagtcccgcaacgagcgcaa 1085

Query: 1080 cccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataaa 1139
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Sbjct: 1086 cccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccagtgataaa 1145

Query: 1140 ccggaggaaggtggggatgacgtcaagtcattcatggcccttacgaccagggctacacacg 1199
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Sbjct: 1146 ctggaggaaggtggggatgacgtcaagtcattcatggcccttacgagtagggctacacacg 1205

Query: 1200 tgctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagt 1259
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Sbjct: 1206 tgctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagt 1265

Query: 1260 gcgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaat 1319
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Sbjct: 1266 gcgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaat 1325

Query: 1320 cgtggatcagaatgccacgggtgaatacgttcccgggccttgtaacacacgcccgtcacac 1379
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Sbjct: 1326 cgtggatcagaatgccacgggtgaatacgttcccgggccttgtaacacacgcccgtcacac 1385

Query: 1380 catgggagtggggtgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccactt 1439
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Sbjct: 1386 catgggagtggggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccactt 1445

Query: 1440 tgtgattcat 1449

|||||

Sbjct: 1446 tgtgattcat 1455

>gi|1857865|gb|U88545.1|STU88545 Salmonella typhi 16S ribosomal RNA gene, comple
Length = 1541

Score = 2547 bits (1285), Expect = 0.0

Identities = 1409/1449 (97%), Gaps = 1/1449 (0%)

Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60

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Query: 61 tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120

|||||

Sbjct: 92 tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 151

Query: 121 ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180

|||||

Sbjct: 152 ctactggaaacggtagctaataccgcataacgtcgcaagaccaaagagggggaccttcgg 211

Query: 181 gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240

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Sbjct: 212 gcctcttgccatcggatgtgccagatgggattagctagtaggtggggtaacggctcacc 271

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300

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Sbjct: 272 taggcgacgatccctagctggtctgagaggatgaccagccacactgaagctgaagcacgg 331

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360

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Sbjct: 332 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 391

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Sbjct: 392 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 451

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcagaagaagcaccggctaact 480

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Sbjct: 452 ggtgttggtggttaataaccgcagcaattgacgttaccgcagaagaagcaccggctaact 511

Query: 481 ccgtgccagcagccgcggtaatacggaggggtgcaagcggttaatcggaattactgggcgta 540

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Sbjct: 512 ccgtgccagcagccgcggtaatacggaggggtgcaagcggttaatcggaattactgggcgta 571

Query: 541 aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct: 572 aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 631

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcggt 660
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Sbjct: 632 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcggt 691

Query: 661 gaaatgcgtagagatctggaggaataccggtggcgaaggcgccccctggacgaagactg 720
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Sbjct: 692 gaaatgcgtagagatctggaggaataccggtggcgaaggcgccccctggacgaagactg 751

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
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Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 900
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Sbjct: 872 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 931

Query: 901 gcacaagcgggtggagcatgtggtttaaattcgatgcaacgcgaagaaccttacctgggtctt 960
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Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
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Sbjct: 992 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1051

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcgcaacgagcgcaac 1080
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Sbjct: 1052 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcgcaacgagcgcaac 1111

Query: 1081 ccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataaac 1140
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Sbjct: 1112 ccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataaac 1171

Query: 1141 cggaggaagggtggggatgacgtcaagtcacatcatggcccttacgaccagggtacacacgt 1200
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Sbjct: 1172 cggaggaagggtggggatgacgtcaagtcacatcatggcccttacgaccagggtacacacgt 1231

Query: 1201 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
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Sbjct: 1232 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1291

Query: 1261 cgtcgtagtccggattggagtctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
 |||||
 Sbjct: 1292 cgtcgtagtccggattggagtctgcaactcgactccatgaagtcggaatcgctagtaatc 1351

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtaacacaccgcccgtcacacc 1380
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 Sbjct: 1352 gtggatcagaatgccacggtgaatacgttcccgggccttgtaacacaccgcccgtcacacc 1411

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
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 Sbjct: 1412 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1471

Query: 1441 gtgattcat 1449
 |||||
 Sbjct: 1472 gtgattcat 1480

>gi|2209047|dbj|AB004755.1| Klebsiella planticola gene for 16S ribosomal RNA, pa
 Length = 1451

Score = 2535 bits (1279), Expect = 0.0
 Identities = 1406/1449 (97%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
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 Sbjct: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagaaagcagcttgctgctt 60

Query: 61 tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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 Sbjct: 61 cgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
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 Sbjct: 121 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 180

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Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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 Sbjct: 241 aaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
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Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
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Sbjct: 421 ggtgntgtggtggttaataaccacagcaattgacgttaccgcgagaagaagcaccggctaact 480

Query: 481 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
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Sbjct: 481 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540

Query: 541 aagcgcacgcagggcggttgattaaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Query: 601 gcatttgaaaactggtcagcttgagtctcgtagaggggggtagaattccagggtgtagcggt 660
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Sbjct: 601 gcatttgataactggcaggcttgagtctcgtagaggggggtagaattccagggtgtagcggt 660

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 720
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Sbjct: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 720

Query: 721 acgctcagggtgcgaaagcggtggggagcaaacaggattagataccctggtagtccacgccg 780
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Sbjct: 721 acgctcagggtgcgaaagcggtggggagcaaacaggattagataccctggtagtccacgccg 780

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Sbjct: 781 taaacgatgtcgacttgagggttggtgcccttgaggcggtggcttccggagctaacgcgtta 840

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Sbjct: 841 agtcgaccgcctggggagtagcggccgcaagggttaaaactcaaataattgacggggggccc 900

Query: 901 gcacaagcggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctgggtctt 960
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Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
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Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
 |||
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 Sbjct: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
 |||
 Sbjct: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440

Query: 1441 gtgattcat 1449
 |||
 Sbjct: 1441 gtgattcat 1449

>gi|18644561|gb|AF371852.1| Uncultured bacterium clone p-2172-s959-3 16S ribosom
 partial sequence
 Length = 1471

Score = 2522 bits (1272), Expect = 0.0
 Identities = 1406/1448 (97%), Gaps = 2/1448 (0%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
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 Sbjct: 26 acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctc 83

Query: 61 tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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 Sbjct: 84 gggtgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 143

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
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 Sbjct: 144 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagaggggggaccttcgg 203

Query: 181 gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 204 gcctcttgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 263

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 264 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 323

Query: 301 tccagactcctacgggagggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 324 tccagactcctacgggagggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 383

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 444 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 503

Query: 481 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
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Sbjct: 564 aagcgcacgcagggcggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 623

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Query: 661 gaaatgcgtagagatctggaggaataccggtggcgaaggcggccccctggacgaagactg 720
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Query: 721 acgctcaggtgcgaaagcggtggggagcaaacaggattagataccctggtagtccacgccg 780
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Sbjct: 744 acgctcaggtgcgaaagcggtggggagcaaacaggattagataccctggtagtccacgccg 803

Query: 781 taaacgatgtcgacttgagggttggtgcccttgaggcggtggcttcggagctaacgcgtta 840
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Query: 901  gcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
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Sbjct: 1164 tggaggaaggtggggatgacgtcaagtcacatggcccttacgagttaggggtacacacgt 1223

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Query: 1441 gtgattca 1448
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>gi|22758972|gb|AF534193.1| Uncultured bacterium clone Caf17 16S ribosomal RNA g
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Length = 1462

Score = 2516 bits (1269), Expect = 0.0
Identities = 1406/1449 (97%), Gaps = 2/1449 (0%)
Strand = Plus / Plus

4/22/03

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Query: 781 taaacgatgtcgacttggaggttgtgcccttgaggcggtggttccggagctaacgcgtta 840
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Query: 841 agtcgaccgcctggggagtacggccgcaagggttaaaactcaaataaattgacggggggccc 900
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Sbjct: 844 agtcgaccgcctggggagtacggccgcaagggttaaaactcaaataaattgacggggggccc 903

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Sbjct: 1384 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1443

Query: 1441 gtgattcat 1449
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Sbjct: 1444 gtgattcat 1452

>gi|29468966|gb|AY217654.1| Escherichia senegalensis 16S ribosomal RNA gene, par
 Length = 1534

Score = 2492 bits (1257), Expect = 0.0
Identities = 1401/1449 (96%)
Strand = Plus / Plus

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Query: 61 tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Sbjct: 266 taggcgacgatccctagccggtctgagaggatgaccagccacactggaactgagacacgg 325

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
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Sbjct: 326 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 385

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
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Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccgggctaact 480
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Sbjct: 446 ggcgtatgcggttaataaccgcgtcgattgacgttaccgcgagaagaagcaccgggctaact 505

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 Sbjct: 1406 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1465

Query: 1441 gtgattcat 1449
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>gi|22758986|gb|AF534207.1| Uncultured bacterium clone Phe11 16S ribosomal RNA g
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 Length = 1462

Score = 2492 bits (1257), Expect = 0.0
 Identities = 1403/1449 (96%), Gaps = 2/1449 (0%)
 Strand = Plus / Plus

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Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
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Query: 1441 gtgattcat 1449
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 Strand = Plus / Plus

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Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 240

4/22/03

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Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
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Sbjct: 632 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 691
|||||

Query: 661 gaaatgcgtagagatctggaggaataaccgggtggcgaaggcgggccccctggacgaagactg 720
|||||

Sbjct: 692 gaaatgcgtagagatctggaggaataaccgggtggcgaaggcgggccccctggacgaagactg 751
|||||

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
|||||

4/22/03

Sbjct: 1472 gtgattcat 1480

>gi|3169774|gb|AF025364.1|AF025364 Citrobacter sedlakii 16S ribosomal RNA gene,
Length = 1522

Score = 2480 bits (1251), Expect = 0.0

Identities = 1399/1449 (96%)

Strand = Plus / Plus

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Query: 1      acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
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Sbjct: 27     acgctggcggcaggcctaacacatgcaagtcgaacggtaacaggaagcagcttgctgctt 86

Query: 61     tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
             |||
Sbjct: 87     cgctgacgagtggcggacgggtgagtaatgtctgggaaactgcccggaggagggggataa 146

Query: 121    ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
             |||
Sbjct: 147    ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 206

Query: 181    gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
             |||
Sbjct: 207    gcctcttgccaccggatgtgcccagatgggattagcttggtgaggttaacggctcacc 266

Query: 241    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
             |||
Sbjct: 267    aaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 326

Query: 301    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
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Sbjct: 327    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 386

Query: 361    agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggggaggaa 420
             |||
Sbjct: 387    agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggggaggaa 446

Query: 421    ggtgttggtggttaataaaccgcagcaattgacgttaccgcgagaagaagcaccgggctaact 480
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Sbjct: 447    gggrrttggtggttaataaaccacagtcattgacgttaccgcgagaagaagcaccgggctaact 506

Query: 481    ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
             |||
Sbjct: 507    ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 566

Query: 541    aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct: 567    aagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 626
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| | | | |
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| Query: | 601 | gcatttgaaactggtcagcttgagctcgtagaggggggtagaattccaggtgtagcggt | 660 |
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| Sbjct: | 627 | gcattcgaaactggcaggcttgagctcgtagaggggggtagaattccaggtgtagcggt | 686 |
| | | | |
| Query: | 661 | gaaatgcgtagagatctggaggaataccggtggcgaaggcgccccctggacgaagactg | 720 |
| | | | |
| Sbjct: | 687 | gaaatgcgtagagatctggaggaataccggtggcgaaggcgccccctggacgaagactg | 746 |
| | | | |
| Query: | 721 | acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg | 780 |
| | | | |
| Sbjct: | 747 | acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg | 806 |
| | | | |
| Query: | 781 | taaacgatgtcgacttggaggttgtgcccttgaggcggtggcttcggagctaacgcgtta | 840 |
| | | | |
| Sbjct: | 807 | taaacgatgtctacttggaggttgtgcccttgaggcggtggcttcggagctaacgcgtta | 866 |
| | | | |
| Query: | 841 | agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataattgacggggggccc | 900 |
| | | | |
| Sbjct: | 867 | agtagaccgcctggggagtagcgccgcaagggttaaaactcaaataattgacggggggccc | 926 |
| | | | |
| Query: | 901 | gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctgggtctt | 960 |
| | | | |
| Sbjct: | 927 | gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctgggtctt | 986 |
| | | | |
| Query: | 961 | gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct | 1020 |
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| Sbjct: | 987 | gacatccacggaagactgcagagatgtggttgtgccttcgggaacctgagacaggtgct | 1046 |
| | | | |
| Query: | 1021 | gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcctcgcaacgagcgcaac | 1080 |
| | | | |
| Sbjct: | 1047 | gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcctcgcaacgagcgcaac | 1106 |
| | | | |
| Query: | 1081 | ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac | 1140 |
| | | | |
| Sbjct: | 1107 | ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccagtgataaac | 1166 |
| | | | |
| Query: | 1141 | cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt | 1200 |
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| Sbjct: | 1167 | tggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt | 1226 |
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| Query: | 1201 | gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg | 1260 |
| | | | |
| Sbjct: | 1227 | gctacaatggcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta | 1286 |
| | | | |
| Query: | 1261 | cgtagtagtccgattggagctctgcaactcgactccatgaagtcggaatcgtagtaatc | 1320 |
| | | | |
| Sbjct: | 1287 | tgtagtagtccgattggagctctgcaactcgactccatgaagtcggaatcgtagtaatc | 1346 |

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtacacaccgcccgtcacacc 1380
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Sbjct: 1347 gtggatcagaatgccacggtgaatacgttcccgggccttgtacacaccgcccgtcacacc 1406

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
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Sbjct: 1407 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1466

Query: 1441 gtgattcat 1449
|||||
Sbjct: 1467 gtgattcat 1475

>gi|2209040|dbj|AB004748.1| Enterobacter gergoviae gene for 16S ribosomal RNA, p
Length = 1450

Score = 2478 bits (1250), Expect = 0.0

Identities = 1399/1449 (96%)

Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
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Sbjct: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtagcagaaagaagcttgcttctt 60

Query: 61 tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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Sbjct: 61 tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 120

Query: 121 ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180
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Sbjct: 121 ctactggaaacggtagctaataccgcataacgtcttcggaccaaagagggggaccttcgg 180

Query: 181 gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
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Sbjct: 181 gcctcttgccatcggatgtgccagatgggattagctagtaggtggggtaacggctcacc 240

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Sbjct: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
|||||
Sbjct: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360

Query: 361 agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggggaggaa 420
|||||
Sbjct: 361 agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggggaggaa 420

4/22/03

Query: 1141 cggaggaaggtggggatgacgtcaagtcatcatggcccttacgaccagggctacacacgt 1200
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Query: 1201 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
 |||||
 Sbjct: 1201 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260

Query: 1261 cgtcgtagtagccggttgaggctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
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 Sbjct: 1261 cgtcgtagtagccggttgaggctgcaactcgactccatgaagtcggaatcgctagtaatc 1320

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
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 Sbjct: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380

Query: 1381 atgggagtaggggtgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
 |||||
 Sbjct: 1381 atgggagtaggggtgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440

Query: 1441 gtgattcat 1449
 |||||
 Sbjct: 1441 gtgattcat 1449

>gi|3169780|gb|AF025370.1|AF025370 Citrobacter amalonaticus 16S ribosomal RNA ge
 Length = 1525

Score = 2476 bits (1249), Expect = 0.0
 Identities = 1399/1449 (96%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
 |||||
 Sbjct: 27 acgctggcggcaggcctaacacatgcaagtcgaacggtaacaggaagcagcttgctgctt 86

Query: 61 tgctgacgagtgccggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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 Sbjct: 87 tgctgacgagtgccggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 146

Query: 121 ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180
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 Sbjct: 147 ctactggaaacggtagctaataccgcataatgtcgcaagaccaaagagggggaccttcgg 206

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 240
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 Sbjct: 207 gcctcttgccatcggatgtgcccagatgggattagctagttggtgaggtaacgggtcacc 266

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
|||||
Sbjct: 267 aaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 326

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
|||||
Sbjct: 327 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 386

Query: 361 agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggggaggaa 420
|||||
Sbjct: 387 agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggggaggaa 446

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
|||
Sbjct: 447 ggggttaagggttaataacccttagccattgacgttaccgcgagaagaagcaccggctaact 506

Query: 481 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
|||||
Sbjct: 507 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 566

Query: 541 aagcgcacgcagggcggttgattaaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct: 567 aagcgcacgcagggcggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 626

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
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Sbjct: 627 gcattcgaaactggcaggcttgagtctcgtagaggggggtagaattccaggtgtagcgg 686

Query: 661 gaaatgcgtagagatctggaggaataccggtggcgaaggcgccccctggacgaagactg 720
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Sbjct: 687 gaaatgcgtagagatctggaggaataccggtggcgaaggcgccccctggacgaagactg 746

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
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Sbjct: 747 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 806

Query: 781 taaacgatgtcgacttgagggttggtgcccttgaggcggtggttcggagctaacgcgtta 840
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Sbjct: 807 taaacgatgtctatttgagggttggtgcccttgaggcggtggttcggagctaacgcgtta 866

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataattgacggggggccc 900
|||
Sbjct: 867 aatagaccgcctggggagtagcgccgcaagggttaaaactcaaataattgacggggggccc 926

Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
|||||
Sbjct: 927 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 986

```

Query: 961  gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
          ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 987  gacatccacagaacttggcagagatgccttggtgccttcgggaactgtgagacaggtgct 1046

Query: 1021 gcatggctgtcgtcagctcgtgtgtgaaatggtgggttaagtcccgcaacgagcgcaac 1080
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1047 gcatggctgtcgtcagctcgtgtgtgaaatggtgggttaagtcccgcaacgagcgcaac 1106

Query: 1081 ccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataaac 1140
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1107 ccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccagtgataaac 1166

Query: 1141 cggaggaaggtggggatgacgtcaagtcatcatggcccttacgaccagggctacacacgt 1200
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1167 tggaggaaggtggggatgacgtcaagtcatcatggcccttacgaccagggctacacacgt 1226

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 1227 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1286

Query: 1261 cgtcgtagtcgggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
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Sbjct: 1287 tgtcgtagtcgggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1346

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
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Sbjct: 1347 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1406

Query: 1381 atgggagtggggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
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Sbjct: 1407 atgggagtggggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1466

Query: 1441 gtgattcat 1449
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>gi|6644288|gb|AF208013.1|AF208013 Enteric Group 137 16S ribosomal RNA gene, par
Length = 1538

Score = 2472 bits (1247), Expect = 0.0
Identities = 1396/1449 (96%)
Strand = Plus / Plus

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Query: 1  acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct: 29  acgctggcggcaggcctaacacatgcaagtcgaacggtaacaggaagcagcttgctgctt 88

Query: 61  tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120

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      |||
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Query: 121  ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
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Sbjct: 149  ctactggaaacggtagctaataaccgcataaaygtcgcaagaccaaagagggggaccttcgg 208

Query: 181  gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
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Sbjct: 209  gcctcttgccatcgatgtgcccagatgggattagcttggttggtgaggtaacggctcacc 268

Query: 241  taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Sbjct: 269  aaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 328

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Query: 361  agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
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Sbjct: 389  agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 448

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Query: 481  ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
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Sbjct: 509  ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 568

Query: 541  aagcgcacgcaggcgggttgattaagtacagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct: 569  aagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 628

Query: 601  gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcggt 660
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Sbjct: 629  gcattcgaaactggcaggcttgagtctcgtagaggggggtagaattccaggtgtagcggt 688

Query: 661  gaaatgcgtagagatctggaggaataaccggtggcgaggcgccccctggacgaagactg 720
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Sbjct: 689  gaaatgcgtagagatctggaggaataaccggtggcgaggcgccccctggacgaagactg 748

Query: 721  acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
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Sbjct: 749  acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 808

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```

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      |||
Sbjct: 869 aatagaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 928

Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
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Sbjct: 929 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 988

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
      |||
Sbjct: 989 gacatccacagaacttggcagagatgccttggtgccttcgggaactgtgagacaggtgct 1048

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1080
      |||
Sbjct: 1049 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1108

Query: 1081 ccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataaac 1140
      |||
Sbjct: 1109 ccttatcctttgttgccagcgrtycggycgggaactcaaaggagactgccagtataaac 1168

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggctacacacgt 1200
      |||
Sbjct: 1169 tggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggctacacacgt 1228

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
      |||
Sbjct: 1229 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1288

Query: 1261 cgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
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Sbjct: 1289 tgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1348

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
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Sbjct: 1349 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1408

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
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Sbjct: 1409 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1468

Query: 1441 gtgattcat 1449
      |||
Sbjct: 1469 gtgattcat 1477
```

>gi|3169773|gb|AF025363.1|AF025363 *Citrobacter rodentium* 16S ribosomal RNA gene,
Length = 1496

Score = 2472 bits (1247), Expect = 0.0

Identities = 1398/1449 (96%)

Strand = Plus / Plus

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Sbjct: 26     acgctggcggcaggcctaacacatgcaagtcgaacggtaacaggaagcagcttgctgctt 85

Query: 61     tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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Sbjct: 86     cgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcccggtggagggggataa 145

Query: 121    ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
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Sbjct: 146    ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 205

Query: 181    gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
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Sbjct: 206    gcctcttgccaccggatgtgccagatgggattagcttgttggtgaggtaacggctcacc 265

Query: 241    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Sbjct: 266    aaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 325

Query: 301    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
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Sbjct: 326    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 385

Query: 361    agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
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Sbjct: 386    agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 445

Query: 421    ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccgggtaact 480
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Sbjct: 446    gggattgtggtggttaataaccgcagtcattgacgttaccgcgagaagaagcaccgggtaact 505

Query: 481    ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
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Sbjct: 506    ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 565

Query: 541    aagcgcacgcaggcgggtgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct: 566    aagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 625

Query: 601    gcatttgaaactgggtcagcttgagtcctcgtagaggggggtagaattccaggtgtagcgg 660
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Sbjct: 626 gcattcgaaactggcaggcttgagtctcgtagaggggggtggaattccagggtgtagcggt 685

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 720
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Sbjct: 686 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 745

Query: 721 acgctcagggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
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Sbjct: 746 acgctcagggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 805

Query: 781 taaacgatgtcgacttggaggttggtgcccttgaggcggtggttccggagctaacgcgtta 840
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Sbjct: 806 taaacgatgtctacttggaggttggtgcccttgaggcggtggttccggagctaacgcgtta 865

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 900
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Sbjct: 866 agtagaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 925

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Sbjct: 986 gacatccagagaactctccagagatgggttggtgccttcgggarctctgagacagggtgct 1045

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Sbjct: 1106 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccagtataaac 1165

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Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
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Sbjct: 1226 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1285

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Sbjct: 1286 tgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1345

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
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Sbjct: 1346 gtggatcagaatgccacggtgaatacgtccccgggccttgtagacacaccgcccgtcacacc 1405

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
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Sbjct: 1406 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1465

Query: 1441 gtgattcat 1449
 |||||

Sbjct: 1466 gtgattcat 1474

>gi|4581981|emb|AJ233408.1|CFR233408 Citrobacter freundii 16S rRNA gene (strain
 Length = 1505

Score = 2468 bits (1245), Expect = 0.0
 Identities = 1398/1449 (96%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
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 Sbjct: 13 acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagaggagcttgctcctt 72

Query: 61 tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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 Sbjct: 73 gggtagcagagtggcggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 132

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
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 Sbjct: 133 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 192

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
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 Sbjct: 193 gcctcttgccatcggatgtgcccagatgggattagctagtaggtggggtaacggctcacc 252

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
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Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
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Query: 421 ggtgttggtgtaataaccgcagcaattgacgttacccgcagaagaagcaccgggtaact 480
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Sbjct: 493 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 552

Query: 541 aagcgcacgcaggcggttgattaaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 720
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Query: 901 gcacaagcggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
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Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
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Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
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Sbjct: 1153 tggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacacgt 1212

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Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggacctgtacacaccgcccgtcacacc 1380
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Sbjct: 1333 gtggatcagaatgccacggtgaatacgttcccgggacctgtacacaccgcccgtcacacc 1392

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
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Sbjct: 1393 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1452

Query: 1441 gtgattcat 1449
          |||
Sbjct: 1453 gtgattcat 1461

```

>[gi|1916302|gb|U92193.1|SBU92193](#) *Salmonella bovis* morbificans 16S ribosomal RNA
sequence
Length = 1541

Score = 2468 bits (1245), Expect = 0.0
Identities = 1399/1449 (96%), Gaps = 1/1449 (0%)
Strand = Plus / Plus

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Sbjct: 33      acgctggcggcaggcctaacacatgcaagtcgaacggtaacaggaagaagcttgct-cgc 91

Query: 61      tgctgacgagtggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
          |||
Sbjct: 92      tgctgacgagtggcgacgggtgcgtaatgtctgggaaactgcctgatggagggggataa 151

Query: 121     ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
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Sbjct: 152     ctactggaaacggtagctaatacccgcataacgtcgcaagaccaaagagggggacctccag 211

Query: 181     gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 240
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Sbjct: 212     gcctcttcccatcgatgtgcccagatgggattagctagttggtgaggttaacgggtcacc 271

Query: 241     taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Sbjct: 272     aaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 331

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Query: 301 tccagactcctacgggaggcagcagtgagggaatattgcacaatgggcgcaagcctgatgc 360
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Sbjct: 332 tccagactcctacgggaggcagcagtgagggaatattgcacagtgtgcgcaagcctgatgc 391

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
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Sbjct: 392 agccatgccgcctgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 451

Query: 421 ggtgttggtgtaataaccgcagcaattgacgttaccgcagaagaagcaccggctaact 480
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Sbjct: 452 ggtgttggtgtaataactgcagcaattgacgttaccgcagaagaagcaccggctaact 511

Query: 481 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
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Sbjct: 512 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 571

Query: 541 aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct: 572 aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 631

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
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Sbjct: 632 gcatttgataactggcaagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 691

Query: 661 gaaatgcgtagagatctggaggaataaccgggtggcgaaggcggccccctggacgaagactg 720
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Sbjct: 692 gaaatgcgtagagatctggaggaataaccgggtggcgaaggcggccccctggacgaagactg 751

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
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Sbjct: 752 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 811

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Query: 841 agtcgaccgcctggggagtagcggccgcaagggttaaaactcaaataattgacggggggccc 900
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Query: 1201 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
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 Sbjct: 1232 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1291

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 Sbjct: 1292 cgtcgtagtcggttgaggatctgcaactcgactccatgaagtcggaatcgctagtaatc 1351

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 Sbjct: 1352 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1411

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
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 Sbjct: 1412 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1471

Query: 1441 gtgattcat 1449
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 Sbjct: 1472 gtgattcat 1480

>gi|3169781|gb|AF025371.1|AF025371 *Citrobacter farmeri* 16S ribosomal RNA gene, p
 Length = 1511

Score = 2466 bits (1244), Expect = 0.0
 Identities = 1397/1449 (96%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
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Query: 61 tgctgacgagtggtggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
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 Sbjct: 74 cgctgacgagtggtggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 133

Query: 121 ctactggaaacggtagctaataaccgcataaacgtctacggaccaaagtgggggaccttcgg 180
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Sbjct: 134 ctactggaaacggtagctaataaccgcataaacgtcgcaagaccaaagagggggaccttcgg 193

Query: 181 gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
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Sbjct: 194 gcctcttgccatcggtatgtgccagatgggattagcttggtggtgaggtaacggctcacc 253

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Sbjct: 254 aaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 313

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
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Sbjct: 314 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 373

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
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Sbjct: 374 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 433

Query: 421 ggtggttggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
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Sbjct: 434 ggggttatggttaataaccttanccattgacgttaccgcgagaagaagcaccggctaact 493

Query: 481 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 540
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Sbjct: 494 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 553

Query: 541 aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct: 554 aagcgcacgcaggcgggtctgtcaagtcggtatgtgaaatccccgggctcaacctgggaact 613

Query: 601 gcatttgaaactggcagcttgagtctcgtagaggggggtagaattccagggtgtagcggt 660
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Sbjct: 614 gcattcgaaactggcaggcttgagtctcgtagaggggggtagaattccagggtgtagcggt 673

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Sbjct: 674 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 733

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
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Sbjct: 734 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 793

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Query: 901 gcacaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctgggtctt 960
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Sbjct: 914 gcacaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctgggtctt 973

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Sbjct: 1034 gcatggctgtcgtcagctcgtgttgtaaattgttgggttaagtcccgcaacgagcgcaac 1093

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Sbjct: 1094 ccttatcctttgttgccagcgggtccggccgggaactcaaaggagactgccagtgataaac 1153

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Sbjct: 1154 tggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccagggctacacacgt 1213

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagt 1260
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Sbjct: 1214 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1273

Query: 1261 cgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
      |||
Sbjct: 1274 tgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1333

Query: 1321 gtggatcagaatgccacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
      |||
Sbjct: 1334 gtggatcagaatgccacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1393

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
      |||
Sbjct: 1394 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1453

Query: 1441 gtgattcat 1449
      |||
Sbjct: 1454 gtgattcat 1462

```

>gi|3169775|gb|AF025365.1|AF025365
Length = 1523

Citrobacter freundii 16S ribosomal RNA gene,

Score = 2464 bits (1243), Expect = 0.0
Identities = 1397/1449 (96%)
Strand = Plus / Plus

```
Query: 1      acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
             |||
Sbjct: 27     acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagaggagcttgctcctt 86

Query: 61     tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
             |||
Sbjct: 87     gggtgacgagtgggcgacgggtgagtaatgtctgggaaactgcccgatggagggggataa 146

Query: 121    ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
             |||
Sbjct: 147    ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 206

Query: 181    gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
             |||
Sbjct: 207    gcctcttgccatcggatgtgcccagatgggattagctagtaggtggggtaacggctcacc 266

Query: 241    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
             |||
Sbjct: 267    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 326

Query: 301    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
             |||
Sbjct: 327    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 386

Query: 361    agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggggaggaa 420
             |||
Sbjct: 387    agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggaggaggaa 446

Query: 421    ggtgttggtggttaataaaccgcagcaattgacgttaccgcagaagaagcaccgggctaact 480
             |||
Sbjct: 447    ggcgttgtggttaataaaccgcagcgattgacgttactcgcagaagaagcaccgggctaact 506

Query: 481    ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 540
             |||
Sbjct: 507    ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 566

Query: 541    aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct: 567    aagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 626

Query: 601    gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccagggtgtagcggt 660
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Sbjct: 627    gcatccgaaactggcaggctagagtctttagaggggggtagaattccagggtgtagcggt 686
```

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 720
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Sbjct: 687 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacaaagactg 746

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
|||||
Sbjct: 747 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 806

Query: 781 taaacgatgtcgacttggaggttgtgcccttgaggcggtggcttccggagctaacgcgtta 840
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Sbjct: 807 taaacgatgtcgacttggaggttgtgcccttgaggcggtggcttccggagctaacgcgtta 866

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 900
|||||
Sbjct: 867 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 926

Query: 901 gcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
|||||
Sbjct: 927 gcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 986

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcttccgggaactctgagacaggtgct 1020
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Sbjct: 987 gacatccagagaacttagcagagatgctttggtgccttccgggaactctgagacaggtgct 1046

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1080
|||||
Sbjct: 1047 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1106

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
|||||
Sbjct: 1107 ccttatcctttgttgccagcggttcggycgggaactcaaaggagactgccagtgataaac 1166

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccagggctacacacgt 1200
|||||
Sbjct: 1167 tggaggaaggtggggatgacgtcaagtcacatcatggcccttacgagtagggctacacacgt 1226

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
|||||
Sbjct: 1227 gctacaatggcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1286

Query: 1261 cgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
|||||
Sbjct: 1287 tgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1346

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
|||||
Sbjct: 1347 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1406

Query: 1381 atgggagtggttgcaaaagaagtaggttagcttaaccttcgggagggcgcttaccacttt 1440
 |||
 Sbjct: 1407 atgggagtggttgcaaaagaagtaggttagcttaaccttcgggagggcgcttaccacttt 1466

Query: 1441 gtgattcat 1449
 |||
 Sbjct: 1467 gtgattcat 1475

>gi|20378116|gb|AF373198.1| Pantoea stewartii subsp. stewartii strain GSPB 2626
 gene, partial sequence
 Length = 1527

Score = 2460 bits (1241), Expect = 0.0
 Identities = 1397/1449 (96%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
 |||
 Sbjct: 27 acgctggcggcaggcctaacacatgcaagtcggacgtagcacagaggagcttgctcctc 86

Query: 61 tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
 |
 Sbjct: 87 gggtagcagagtggcggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 146

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
 |||
 Sbjct: 147 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagtgggggacctccgg 206

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
 |||
 Sbjct: 207 gcctcacaccatcggatgtgcccagatgggattagctagtaggcggggtaacggcccacc 266

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
 |||
 Sbjct: 267 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 326

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
 |||
 Sbjct: 327 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 386

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
 |||
 Sbjct: 387 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 446

Query: 421 ggtgttggtggttaataaaccgcagcaattgacgttaccgcgagaagaagcaccgggctaact 480
 |||
 Sbjct: 447 ggtggtgaggttaataaacctcatcaattgacgttaccgcgagaagaagcaccgggctaact 506

Query: 481 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
|||||
Sbjct: 507 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 566

Query: 541 aagcgcacgcagcggttgattaaagtcagatgtgaaatccccgggctcaacctgggaact 600
|||||
Sbjct: 567 aagcgcacgcagcggtctgttaagtcagatgtgaaatccccgggcttaacctgggaact 626

Query: 601 gcatttgaaactggtcagcttgagctctcgtagaggggggtagaattccagggtgtagcggt 660
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Sbjct: 627 gcatttgaaactggcaggcttgagctctcgtagaggggggtagaattccagggtgtagcggt 686

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaaggcgccccctggacgaagactg 720
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Sbjct: 687 gaaatgcgtagagatctggaggaataaccggtggcgaaaggcgccccctggacgaagactg 746

Query: 721 acgctcagggtgcgaaagcggtggggagcaaacaggattagataccctggtagtccacgccg 780
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Sbjct: 747 acgctcagggtgcgaaagcggtggggagcaaacaggattagataccctggtagtccacgccg 806

Query: 781 taaacgatgtcgacttggaggttgtgcccttgaggcggtggttccggagctaacgcgtta 840
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Sbjct: 807 taaacgatgtcgacttggaggttgttcccttgaggagtggttccggagctaacgcgtta 866

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 900
|||||
Sbjct: 867 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 926

Query: 901 gcacaagcggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
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Sbjct: 927 gcacaagcggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 986

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacagggtgct 1020
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Sbjct: 987 gacatccagcgaacttggcagagatgccttgggtgccttcgggaacgctgagacagggtgct 1046

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaagttgggttaagtcccgcaacgagcgcaac 1080
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Sbjct: 1047 gcatggctgtcgtcagctcgtgttgtaaagttgggttaagtcccgcaacgagcgcaac 1106

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
|||||
Sbjct: 1107 ccttatcctttgttgccagcgattcggtcgggaactcaaaggagactgccggtgataaac 1166

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
|||||
Sbjct: 1167 cggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacacgt 1226

Query: 1201 gctacaatggcgcatatacaaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
|||||
Sbjct: 1227 gctacaatggcgcatatacaaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1286

Query: 1261 cgtcgtagtagccggttgaggatctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
|||||
Sbjct: 1287 cgtcgtagtagccggttgaggatctgcaactcgactccgtagaagtcggaatcgctagtaatc 1346

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
|||||
Sbjct: 1347 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1406

Query: 1381 atgggagtaggggtgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
|||||
Sbjct: 1407 atgggagtaggggtgcaaaagaagtaggtagcttaacccccgggagggcgcttaccacttt 1466

Query: 1441 gtgattcat 1449
|||||
Sbjct: 1467 gtgattcat 1475

>gi|4581997|emb|AJ233410.1|EAM233410 Erwinia amylovora 16S rRNA gene (strain DSM
Length = 1497

Score = 2460 bits (1241), Expect = 0.0
Identities = 1399/1449 (96%), Gaps = 2/1449 (0%)
Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
|||||
Sbjct: 13 acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctt 70

Query: 61 tgctgacgagtgccggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
|||||
Sbjct: 71 gggtagcagagtgccggacgggtgagtaatgtctgggaaactgccgatggagggggataa 130

Query: 121 ctactggaaacggtagcttaataccgcataacgtctacggaccaaagtgggggaccttcgg 180
|||||
Sbjct: 131 ctactggaaacggtagcttaataccgcataacgtctacggaccaaagtgggggaccttcgg 190

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 240
|||||
Sbjct: 191 gcctcacaccatcggtatgtgcccagatgggattagctggttaggtggggtaacgggtcacc 250

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
|||||
Sbjct: 251 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 310

Query: 301 tccagactcctacgggagggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360

4/22/03


```

      |||
Sbjct: 1031 gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcgcaacgagcgcaac 1090

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
      |||
Sbjct: 1091 ccttatcctttgttgccagcgattcggtcggaactcaaaggagactgccggtgataaac 1150

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccagggctacacacgt 1200
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Sbjct: 1151 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccagggctacacacgt 1210

Query: 1201 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
      |||
Sbjct: 1211 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1270

Query: 1261 cgtcgtagtcggttggagtcgcaactcgactccatgaagtcggaatcgctagtaatc 1320
      |||
Sbjct: 1271 cgtcgtagtcggttggagtcgcaactcgactccgtagaagtcggaatcgctagtaatc 1330

Query: 1321 gtggatcagaatgccacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
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Sbjct: 1331 gtagatcagaatgctacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1390

Query: 1381 atgggagtggttgcaaaaagaagtaggttagcttaaccttcgggagggcgcttaccacttt 1440
      |||
Sbjct: 1391 atgggagtggttgcaaaaagaagtaggttagcttaaccttcgggagggcgcttaccacttt 1450

Query: 1441 gtgattcat 1449
      |||
Sbjct: 1451 gtgattcat 1459

```

>gi|3169779|gb|AF025369.1| Citrobacter sp. 'genomospecies 11' 16S ribosomal RNA
sequence
Length = 1530

Score = 2460 bits (1241), Expect = 0.0
Identities = 1397/1449 (96%)
Strand = Plus / Plus

```

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
      |||
Sbjct: 27 acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagaggagcttgctcctt 86

Query: 61 tgctgacgagtgccggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
      |||
Sbjct: 87 gggtagcagtgccggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 146

Query: 121 ctactggaaacggtagctaataccgcataacgtctacggaccaaaagtgggggaccttcgg 180

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Sbjct: 147 ||||| ctactggaaacggtagctaataaccgcataaacgtcgcaagaccaaagagggggaccttcgg 206

Query: 181 gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
|||||

Sbjct: 207 gcctcttgccatcggatgtgccagatgggattagctagtaggtggggtaacggctcacc 266

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
|||||

Sbjct: 267 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 326

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
|||||

Sbjct: 327 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 386

Query: 361 agccatgccgcgtgtatgaagaaggccttcggggtgttaaagtactttcagcggggaggaa 420
|||||

Sbjct: 387 agccatgccgcgtgtatgaagaaggccttcggggtgttaaagtactttcagcggaggaggaa 446

Query: 421 ggtgttggtggttaataaaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
|||||

Sbjct: 447 ggtgttgagggttaataaacctcagcaattgacgttactcgcaagaagaagcaccggctaact 506

Query: 481 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
|||||

Sbjct: 507 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 566

Query: 541 aagcgcacgcagggcggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
|||||

Sbjct: 567 aagcgcacgcagggcggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 626

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
|||||

Sbjct: 627 gcacccgaaactggcaggctagagtcttgtagaggggggtagaattccaggtgtagcgg 686

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcggaaggcgccccctggacgaagactg 720
|||||

Sbjct: 687 gaaatgcgtagagatctggaggaataaccggtggcggaaggcgccccctggacaaagactg 746

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
|||||

Sbjct: 747 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 806

Query: 781 taaacgatgtcgacttgagggttggtcccttgaggcggttccggagctaacgcgtta 840
|||||

Sbjct: 807 taaacgatgtcgacttgagggttggtcccttgaggcggttccggagctaacgcgtta 866

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatgaattgacggggggccc 900

```

      |||
Sbjct: 867 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatgaattgacggggggccc 926

Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
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Sbjct: 927 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 986

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
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Sbjct: 987 gacatccagagaacttagcagagatgctttggtgccttcgggaactctgagacaggtgct 1046

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1080
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Sbjct: 1047 gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1106

Query: 1081 ccttatcctttgttgccagcgggtccggccgggaactcaaaggagactgccggtgataaac 1140
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Sbjct: 1107 ccttatcctttgttgccagcgggtccggccgggaactcaaaggagactgccagtataaac 1166

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
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Sbjct: 1167 tggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacacgt 1226

Query: 1201 gctacaatggcgcatatacaaaagagaagcgacctcgcgagagcaagcggacctcataaagt 1260
      |||
Sbjct: 1227 gctacaatggcgcatatacaaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1286

Query: 1261 cgtcgtagtagcggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
      |||
Sbjct: 1287 tgtcgtagtagcggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1346

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
      |||
Sbjct: 1347 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1406

Query: 1381 atgggagtggttgcaaaagaagtaggttagcttaaccttcgggagggcgcttaccacttt 1440
      |||
Sbjct: 1407 atgggagtggttgcaaaagaagtaggttagcttaaccttcgggagggcgcttaccacttt 1466

Query: 1441 gtgattcat 1449
      |||
Sbjct: 1467 gtgattcat 1475

```

>gi|13873050|gb|AF141895.1|AF141895 Erwinia amylovora strain BC204 16S ribosomal
Length = 1480

Score = 2456 bits (1239), Expect = 0.0
Identities = 1398/1449 (96%), Gaps = 2/1449 (0%)

Strand = Plus / Plus

```

Query: 1      acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
              |||
Sbjct: 3      acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctt 60

Query: 61     tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
              |
Sbjct: 61     gggtgacgagtgggcgacgggtgagtaatgtctgggaaactgcccgatggagggggataa 120

Query: 121    ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
              |||
Sbjct: 121    ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180

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Query: 241    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Query: 301    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
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Query: 361    agccatgccgcgtgtatgaagaaggccttcggggttgtaaagtactttcagcggggaggaa 420
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Sbjct: 421    ggggaagaggttaataaccttttcattgacgttaccgcgagaagaagcaccggctaact 480

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Query: 541    aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct: 541    aagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggcttaacctgggaact 600

Query: 601    gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
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Sbjct: 601    gcattcgaaactggcaggctagagtctcgtagaggggggtagaattccaggtgtagcgg 660

Query: 661    gaaatgcgtagagatctggaggaataaccgggtggcgaaggcgccccctggacgaagactg 720
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Sbjct: 661 gaaatgcgtagagatctggaggaataaccggtggcggaaggcgccccctggacgaagactg 720

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Query: 781 taaacgatgtcgacttggaggttggtcccttgaggcggttccggagctaacgcgtta 840
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Sbjct: 781 taaacgatgtcgacttggaggttggtcccttgaggagtggttccggagctaacgcgtta 840

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataattgacggggggccc 900
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Sbjct: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataattgacggggggccc 900

Query: 901 gcacaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctgggtctt 960
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Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggctacacacgt 1200
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Sbjct: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggctacacacgt 1200

Query: 1201 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
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Sbjct: 1201 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260

Query: 1261 cgtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
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Sbjct: 1261 cgtcgtagtccggatcgagctctgcaactcgactccgtgaagtcggaatcgctagtaatc 1320

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
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Sbjct: 1321 gtagatcagaatgctacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
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Sbjct: 1381 atgggagtggttgcaaaagaagtaggttagcttaaccttcgggagggcgcttaccacttt 1440

Query: 1441 gtgattcat 1449

|||||||

Sbjct: 1441 gtgattcat 1449

>gi|3169783|gb|AF025373.1|AF025373 Citrobacter werkmanii 16S ribosomal RNA gene,
Length = 1521

Score = 2454 bits (1238), Expect = 0.0

Identities = 1393/1446 (96%)

Strand = Plus / Plus

Query: 4 ctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctctgc 63

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Query: 64 tgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataacta 123

Sbjct: 84 tgacgagtggcggacgggtgagtaatgtctgggaaactgcccgatggagggggataacta 143

Query: 124 ctggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcggggc 183

Sbjct: 144 ctggaaacggtagctaataccgcataatgtcgaagaccaaagagggggaccttcggggc 203

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Sbjct: 204 tcttgccatcggatgtgcccagatgggattagcttgttaggtggggtaacggctcacctag 263

Query: 244 gcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgggtcc 303

Sbjct: 264 gcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgggtcc 323

Query: 304 agactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgcagc 363

Sbjct: 324 agactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgcagc 383

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Sbjct: 444 gttgtggttaataaccacagcaattgacgttactcgcagaagaagcaccgggctaactccg 503

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Sbjct: 504 tgccagcagccgcggtaataacggaggggtgcaagcggttaatcggaattactgggcgtaaag 563

4/22/03

Query: 1264 cgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatcgtg 1323
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 Sbjct: 1284 cgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatcgtg 1343

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 Sbjct: 1344 gatcagaatgccacggtgaatacgttcccgggccttgtaacacaccgcccgtcacaccatg 1403

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 Sbjct: 1404 ggagtgggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccactttgtg 1463

Query: 1444 attcat 1449
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>gi|13873049|gb|AF141894.1|AF141894 Erwinia amylovora strain BC203 16S ribosomal
 Length = 1480

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 Identities = 1397/1449 (96%), Gaps = 2/1449 (0%)
 Strand = Plus / Plus

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 Sbjct: 3 acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctt 60

Query: 61 tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
 |
 Sbjct: 61 gggtagcagagtgggcgacgggtgagtaatgtctgggaaactgcccgatggagggggataa 120

Query: 121 ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180
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 Sbjct: 121 ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
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 Sbjct: 181 gcctcacaccatcgatgtgcccagatgggattagctggttaggtggggtaacggctcacc 240

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
 |||||
 Sbjct: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
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 Sbjct: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
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Sbjct: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
|| |
Sbjct: 421 gggkragagggttaataacctyctgcattgacgttaccgcgagaagaagcaccggctaact 480

Query: 481 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 540
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Sbjct: 481 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 540

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Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaggcgccccctggacgaagactg 720
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Sbjct: 661 gaaatgcgtagagatctggaggaataaccggtggcgaggcgccccctggacgaagactg 720

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 Sbjct: 1321 gtagatcagaatgctacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380

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 Sbjct: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440

Query: 1441 gtgattcat 1449
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 Sbjct: 1441 gtgattcat 1449

>gi|11907474|emb|AJ277977.1|LAD277977 Leclercia adecarboxylata 16S rRNA gene, st
 Length = 1447

Score = 2452 bits (1237), Expect = 0.0
 Identities = 1399/1448 (96%), Gaps = 5/1448 (0%)
 Strand = Plus / Plus

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 Sbjct: 1 cgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctcg 58

Query: 62 gctgacgagtgccggacgggtgagtaatgtctgggaaactgcctgatggagggggataac 121
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 Sbjct: 59 ggtgacgagtgccggacgggtgagtaatgtctgggaaactgcctgatggagggggataac 118

Query: 122 tactggaaacggtagctaataccgcataacgtctacggaccaaagtggggggaccttcggg 181
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 Sbjct: 119 tactggaaacggtagctaataccgcataacgtcgcaagaccaaagagggggaccttcggg 178

Query: 182 cctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacct 241
|||||
Sbjct: 179 cctcttgccatcagatgtgccagatgggattagctagtaggtggggtaatggctcacct 238

Query: 242 aggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacggt 301
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Sbjct: 239 aggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacggt 298

Query: 302 ccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgca 361
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Sbjct: 299 ccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgca 358

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Query: 482 cgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgtaa 541
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Sbjct: 539 agcgcacgcaggcggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaactg 598

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Query: 722 cgctcaggtgcgaaagcggtggggagcaaacaggattagataccctggtagtccacgccgt 781
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Query: 962  acatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgctg 1021
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Sbjct: 959  acatccagagaacttagcagagatgctttggtgccttcgggaactctgagacaggtgctg 1018

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Sbjct: 1019 catggctgtcgtcagctcgtgttgtaaagtgttggttaagtcgccgcaacgagcgcaacc 1078

Query: 1082 cttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaacc 1141
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Sbjct: 1139 ggaggaaggtggggatgacgtcaagtcacatcatggcccttacgagtagggctacacacgtg 1198

Query: 1202 ctacaatggcgcatacaaaagagaagcgacctcgcgagagcaagcggacctcataaagtgc 1261
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Query: 1262 gtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatcg 1321
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1259 gtcgtagtccggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatcg 1318

Query: 1322 tggatcagaatgccacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacca 1381
          || |||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct: 1319 tagatcagaatgctacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacca 1378

Query: 1382 tgggagtggggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccactttg 1441
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Sbjct: 1379 tgggagtggggttgcaaaagaagtaggtagcttaaccttcgg--aggcgc-taccactttg 1435

Query: 1442 tgattcat 1449
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Sbjct: 1436 tgattcat 1443

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>gi|3169778|gb|AF025368.1|AF025368 Citrobacter braakii 16S ribosomal RNA gene, p
Length = 1530

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Identities = 1396/1449 (96%)
Strand = Plus / Plus

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Sbjct: 87  gggtgacgagtggcggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 146

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Sbjct: 147 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 206

Query: 181 gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
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Sbjct: 207 gcctcttgccatcggatgtgccagatgggattagctagtaggtggggtaacggctcacc 266

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Sbjct: 327 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 386

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          |||
Sbjct: 507 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 566

Query: 541 aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
          |||
Sbjct: 567 aagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 626

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcggt 660
          |||
Sbjct: 627 gcattcgaaactggcaggctagagtcttgtagaggggggtagaattccaggtgtagcggt 686

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcggccccctggacgaagactg 720
          |||
Sbjct: 687 gaaatgcgtagagatctggaggaataaccggtggcgaaggcggccccctggacaaagactg 746

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
```

Sbjct: 747 |||||acgctcaggtgCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCG 806

Query: 781 taaacgatgtcgacttgaggttgTGCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTA 840
|||||

Sbjct: 807 taaacgatgtcgacttgaggttgTGCCTTGAGGCGTGGCTTCCGGAGCTAACGCGTTA 866
|||||

Query: 841 agtcgaccgcctggggagtacggccgcaaggTTAAAACCTCAAATGAATTGACGGGGGGCCC 900
|||||

Sbjct: 867 agtcgaccgcctggggagtacggccgcaaggTTAAAACCTCAAATGAATTGACGGGGGGCCC 926
|||||

Query: 901 gcacaagcggTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTGGTCTT 960
|||||

Sbjct: 927 gcacaagcggTGGAGCATGTGTTTAATTCGATGCAACGCGAAGAACCTTACCTACTCTT 986
|||||

Query: 961 gacatccagagaatcctgcagagatgcgggagTGCCTTCGGGAACCTCTGAGACAGGTGCT 1020
|||||

Sbjct: 987 gacatccagagaacttagcagagatgctttgTGCCTTCGGGAACCTCTGAGACAGGTGCT 1046
|||||

Query: 1021 gcatggctgtcgTcagctcgTgttgTGAATGTTGGGTAAAGTCCCGCAACGAGCGCAAC 1080
|||||

Sbjct: 1047 gcatggctgtcgTcagctcgTgttgTGAATGTTGGGTAAAGTCCCGCAACGAGCGCAAC 1106
|||||

Query: 1081 ccttatcctttgttgccagcggTTCGGCCGGGAACCTCAAAGGAGACTGCCGGTGATAAAC 1140
|||||

Sbjct: 1107 ccttatcctttgttgccagcggTTCGGCCGGGAACCTCAAAGGAGACTGCCAGTGATAAAC 1166
|||||

Query: 1141 cggaggaaggtggggatgacgtcaagTcatcatggccctTACGACCAGGGGTACACACGT 1200
|||||

Sbjct: 1167 tggaggaaggtggggatgacgtcaagTcatcatggccctTACGAGTAGGGGTACACACGT 1226
|||||

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtG 1260
|||||

Sbjct: 1227 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1286
|||||

Query: 1261 cgtcgtagTccggttgagTctgcaactcgactccatgaagTcggaatcgctagtaatc 1320
|||||

Sbjct: 1287 tgtcgtagTccggttgagTctgcaactcgactccatgaagTcggaatcgctagtaatc 1346
|||||

Query: 1321 gtggatcagaatgccacggtgaatacgTtcccgggccttgTACACACCGCCCGTCACACC 1380
|||||

Sbjct: 1347 gtggatcagaatgccacggtgaatacgTtcccgggccttgTACACACCGCCCGTCACACC 1406
|||||

Query: 1381 atgggagTgggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
|||||

Sbjct: 1407 atgggagTgggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1466
|||||

Query: 1441 gtgattcat 1449

|||||||
Sbjct: 1467 gtgattcat 1475

>gi|4581973|emb|AJ233403.1|BGA233403 Buttiauxella gaviniae 16S rRNA gene (strain
Length = 1495

Score = 2448 bits (1235), Expect = 0.0
Identities = 1398/1451 (96%), Gaps = 6/1451 (0%)
Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggta--acagggagcagcttgctgc 58
|||||||
Sbjct: 10 acgctggcggcaggcctaacacatgcaagtcgagcggtagcacagggagcttgctcctg- 68

Query: 59 tctgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggat 118
| |||||
Sbjct: 69 ---ggtgacgagcggcggacgggtgagtaatgtctgggaaactgcctgatggagggggat 125

Query: 119 aactactggaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttc 178
|||||||
Sbjct: 126 aactactggaacggtagctaataaccgcataacgtcttcggaccaaagagggggaccttc 185

Query: 179 gggcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctca 238
|||||||
Sbjct: 186 gggcctcctgccatcagatgtgccagatgggattagctagtaggtgaggtaatggctca 245

Query: 239 cctaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacac 298
|||||||
Sbjct: 246 cctaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacac 305

Query: 299 ggtccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgat 358
|||||||
Sbjct: 306 ggtccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgat 365

Query: 359 gcagccatgccgctgtatgaagaaggccttcgggttgtaaagtactttcagcggggagg 418
|||||||
Sbjct: 366 gcagccatgccgctgtatgaagaaggccttcgggttgtaaagtactttcagcggaggagg 425

Query: 419 aaggtgttggtgtaataaaccgcagcaattgacgttaccgcagaagaagcaccgggctaa 478
|||||
Sbjct: 426 aaggcattgtggtgtaataaaccgcagtgattgacgttactcgcagaagaagcaccgggctaa 485

Query: 479 ctccgtgccagcagccgcggtaataacggagggtgcaagcggttaatcggaattactgggcg 538
|||||||
Sbjct: 486 ctccgtgccagcagccgcggtaataacggagggtgcaagcggttaatcggaattactgggcg 545

Query: 539 taaagcgcacgcaggcgggttgattaaagtcagatgtgaaatccccgggctcaacctgggaa 598
|||||||

4/22/03

Sbjct: 1266 tgcgtcgtagtcggtatcggtgagctgcaactcgactccgtgaagtcggaatcgctagtaa 1325

Query: 1319 tcgtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcaca 1378

|||||

Sbjct: 1326 tcgtagatcagaatgctacggtgaatacgttcccgggccttgtagacacaccgcccgtcaca 1385

Query: 1379 ccatgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccact 1438

|||||

Sbjct: 1386 ccatgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccact 1445

Query: 1439 ttgtgattcat 1449

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Sbjct: 1446 ttgtgattcat 1456

>gi|14549203|dbj|AB053117.1| Klebsiella oxytoca gene for 16S rRNA

Length = 1492

Score = 2448 bits (1235), Expect = 0.0

Identities = 1397/1449 (96%), Gaps = 2/1449 (0%)

Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60

|||||

Sbjct: 25 acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctc 82

Query: 61 tgctgacgagtggtgggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120

|||||

Sbjct: 83 ggggtgacgagtggtgggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 142

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180

|||||

Sbjct: 143 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 202

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240

|||||

Sbjct: 203 gcctcttgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 262

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300

|||||

Sbjct: 263 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 322

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360

|||||

Sbjct: 323 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 382

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420

|||||

Sbjct: 383 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 442

4/22/03

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggctacacacgt 1200
 |||
 Sbjct: 1163 tggaggaaggtggggatgacgtcaagtcacatggcccttacgagtagggctacacacgt 1222

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
 |||
 Sbjct: 1223 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1282

Query: 1261 cgtcgtagtagccggttgaggatctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
 |||
 Sbjct: 1283 tgtcgtagtagccggttgaggatctgcaactcgactccatgaagtcggaatcgctagtaatc 1342

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
 |||
 Sbjct: 1343 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1402

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
 |||
 Sbjct: 1403 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1462

Query: 1441 gtgattcat 1449
 |||
 Sbjct: 1463 gtgattcat 1471

>gi|11907475|emb|AJ277978.1|LAD277978 Leclercia adecarboxylata 16S rRNA gene, st
 Length = 1437

Score = 2444 bits (1233), Expect = 0.0
 Identities = 1390/1437 (96%), Gaps = 4/1437 (0%)
 Strand = Plus / Plus

Query: 2 cgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctct 61
 |||
 Sbjct: 1 cgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctcg 58

Query: 62 gctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataac 121
 |
 Sbjct: 59 ggtgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataac 118

Query: 122 tactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcggg 181
 |||
 Sbjct: 119 tactggaaacggtagctaataccgcataacgtcgcaagaccaaagagggggaccttcggg 178

Query: 182 cctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacct 241
 |||
 Sbjct: 179 cctcttgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacct 238

Query: 242 aggcgacgatccctagct-ggtctgagaggatgaccagccacactggaactgagacacgg 300
|||||
Sbjct: 239 aggcgacgatccctagcttggctgagaggatgaccagccacactggaactgagacacgg 298

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
|||||
Sbjct: 299 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 358

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
|||||
Sbjct: 359 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 418

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
|||||
Sbjct: 419 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 478

Query: 481 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 540
|||||
Sbjct: 479 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 538

Query: 541 aagcgcacgcaggcggttgattaaagtcagatgtgaaatccccgggctcaacctgggaact 600
|||||
Sbjct: 539 aagcgcacgcaggcggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 598

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
|||||
Sbjct: 599 gcattcgaaactggcaggctagagtcttgtagaggggggtagaattccaggtgtagcgg 658

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaggcgccccctggacgaagactg 720
|||||
Sbjct: 659 gaaatgcgtagagatctggaggaataaccggtggcgaggcgccccctggacaaagactg 718

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
|||||
Sbjct: 719 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 778

Query: 781 taaacgatgtcgacttggaggttggtcccttgaggcggtggttccggagctaacgcgtta 840
|||||
Sbjct: 779 taaacgatgtcgacttggaggttggtcccttgaggagtggttccggagctaacgcgtta 838

Query: 841 agtcgaccgcctggggagtacggccgcaagggttaaaactcaaatagaattgacggggggccc 900
|||||
Sbjct: 839 agtcgaccgcctggggagtacggccgcaagggttaaaactcaaatagaattgacggggggccc 898

Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtcctt 960
|||||
Sbjct: 899 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactcctt 958

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Query: 961  gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
          |||
Sbjct: 959  gacatccagagaacttagcagagatgctttggtgccttcgggaactctgagacaggtgct 1018

Query: 1021  gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1080
          |||
Sbjct: 1019  gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1078

Query: 1081  ccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataaac 1140
          |||
Sbjct: 1079  ccttatcctttgttgccagcgggttaggccgggaactcaaaggagactgccagtataaac 1138

Query: 1141  cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
          |||
Sbjct: 1139  tggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacacgt 1198

Query: 1201  gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
          |||
Sbjct: 1199  gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1258

Query: 1261  cgtcgtagtcaggattggagctctgcaactcgactccatgaa-gtcggaatcgctagtaat 1319
          |||
Sbjct: 1259  cgtcgtagtcaggattggagctctgcaactcgactccatgaagggtcggaatcgctagtaat 1318

Query: 1320  cgtggatcagaatgccacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacac 1379
          |||
Sbjct: 1319  cgtagatcagaatgctacggtgaatacgttcccgggccttgtagacacaccgcccgtcacac 1378

Query: 1380  catgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttacca 1436
          |||
Sbjct: 1379  catgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttacca 1435

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>gi|2584810|emb|Z96080.1|PSZ96080 Pantoea stewartii LMG 2715 16S ribosomal RNA
Length = 1497

Score = 2444 bits (1233), Expect = 0.0
Identities = 1393/1449 (96%)
Strand = Plus / Plus

```

Query: 1  acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
          |||
Sbjct: 6  acgctggcggcaggcctaacacatgcaagtcggacggtagcacagaggagcttgctcctc 65

Query: 61  tgctgacgagtggtggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
          |||
Sbjct: 66  gggtagcagagtggtggcgacgggtgagtaatgtctgggaaactgcccgatggagggggataa 125

```

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
|||||
Sbjct: 126 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagtgggggacctccgg 185

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
|||||
Sbjct: 186 gcctcacaccatcggtatgtgcccagatgggattagctagtaggcgggtaacggcccacc 245

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
|||||
Sbjct: 246 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 305

Query: 301 tccagactcctacgggaggcagcagtggggaatatgtcacaaatgggcgcaagcctgatgc 360
|||||
Sbjct: 306 tccagactcctacgggaggcagcagtggggaatatgtcacaaatgggcgcaagcctgatgc 365

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
|||||
Sbjct: 366 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcgggrraggaa 425

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
|||||
Sbjct: 426 ggtggtgaggttaataacctcatcaattgacgttaccgcgagaaraagcaccggctaact 485

Query: 481 ccgtgccagcagccgcggtataacggagggtgcaagcggttaatcggaattactgggcgta 540
|||||
Sbjct: 486 ccgtgccagcagccgcggtataacggagggtgcaagcggttaatcggaattactgggcgta 545

Query: 541 aagcgcacgcaggcggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
|||||
Sbjct: 546 aagcgcacgcaggcggtctgttaagtcagatgtgaaatccccgggcttaacctgggaact 605

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccagggtgtagcggt 660
|||||
Sbjct: 606 gcatttgaaactggcaggcttgagtctcgtagaggggggtagaattccagggtgtagcggt 665

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 720
|||||
Sbjct: 666 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 725

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
|||||
Sbjct: 726 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 785

Query: 781 taaacgatgtcgacttgagggttggtcccttgaggcggtggttccggagctaacgcgtta 840
|||||
Sbjct: 786 taaacgatgtcgacttgagggttggtcccttgaggagtggttccggagctaacgcgtta 845

```

Query: 841  agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 900
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 846  agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 905

Query: 901  gcacaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctgggtctt 960
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 906  gcacaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 965

Query: 961  gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
          ||||||||| ||| ||||||||| |||||||||||||||||||||||||||||||
Sbjct: 966  gacatccagcgaacttggcagagatgccttggtgccttcgggaacgctgagacaggtgct 1025

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaagtgttgggttaagtcccgcaacgagcgcaac 1080
          ||||||||| ||| ||||||||| |||||||||||||||||||||||||||||||
Sbjct: 1026 gcatggctgtcgtcagctcgtgttgtaaagtgttgggttaagtcccgcaacgagcgcaac 1085

Query: 1081 ccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataaac 1140
          ||||||||| ||| ||||||||| |||||||||||||||||||||||||||||||
Sbjct: 1086 ccttatcctttgttgccagcgattcggtagcgggaactcaaaggagactgccggtgataaac 1145

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
          ||||||||| ||| ||||||||| |||||||||||||||||||||||||||||||
Sbjct: 1146 cggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacacgt 1205

Query: 1201 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagt 1260
          ||||||||| ||| ||||||||| |||||||||||||||||||||||||||||||
Sbjct: 1206 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaastg 1265

Query: 1261 cgtcgtagtccggattggagtcgtgcaactcgactccatgaagtcggaatcgctagtaatc 1320
          ||||||||| ||| ||||||||| |||||||||||||||||||||||||||||||
Sbjct: 1266 cgtcgtagtccggatcgagtcgtgcaactcgactccgtgaagtcggaatcgctagtaatc 1325

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
          ||||||||| ||| ||||||||| |||||||||||||||||||||||||||||||
Sbjct: 1326 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1385

Query: 1381 atgggagtggttgcaaaagaagtaggttagcttaaccttcgggagggcgcttaccacttt 1440
          ||||||||| ||| ||||||||| |||||||||||||||||||||||||||||||
Sbjct: 1386 atgggagtggttgcaaaagaagtaggttagcttaacccccgggagggcgcttaccacttt 1445

Query: 1441 gtgattcat 1449
          |||||||||
Sbjct: 1446 gtgattcat 1454

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>gi|3218459|emb|X83265.1|EA16SRR E.amylovora 16S rRNA gene
Length = 1502

Score = 2444 bits (1233), Expect = 0.0

Identities = 1398/1449 (96%), Gaps = 3/1449 (0%)
Strand = Plus / Plus

```
Query: 1      acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
             |||
Sbjct: 26     acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctt 83

Query: 61     tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
             |
Sbjct: 84     gggtgacgagtgggcgacgggtgagtaatgtctgggaaactgcccgatggagggggataa 143

Query: 121    ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180
             |||
Sbjct: 144    ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 203

Query: 181    gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
             |||
Sbjct: 204    gcctcacaccatcggatgtgcccagatgggattagctagtaggtggggtaacggctcacc 263

Query: 241    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
             |||
Sbjct: 264    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 323

Query: 301    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
             |||
Sbjct: 324    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 383

Query: 361    agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
             |||
Sbjct: 384    agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 443

Query: 421    ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
             ||
Sbjct: 444    ggggaagaggttaataaccttttccattgacgttaccgcgagaagaagcaccggctaact 503

Query: 481    ccgtgccagcagccgcggtaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
             |||
Sbjct: 504    ccgtgccagcagccgcggtaatacggaggggtgcaagcggttaatcggaattactgggcgta 563

Query: 541    aagcgcacgcaggcgggtgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
             |||
Sbjct: 564    aagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggcttaacctgggaact 623

Query: 601    gcatttgaaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
             |||
Sbjct: 624    gcattcgaaaactggcaggctagagtctcgtagaggggggtagaattccaggtgtagcgg 683

Query: 661    gaaatgcgtagagatctggaggaataaccgggtggcgaaggcggccccctggacgaagactg 720
```


Sbjct: 684 ||||| gaaatgcgtagagatctggaggaataaccggtggcggaaggcgccccctggacgaagactg 743

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
|||||

Sbjct: 744 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 803

Query: 781 taaacgatgtcgacttggagggtgtgcccttgaggcgtggcttccggagctaacgcgtta 840
|||||

Sbjct: 804 taaacgatgtcgacttggagggtgttcccctgaggagtggcttccggagctaacgcgtta 863

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataaattgacggggggccc 900
|||||

Sbjct: 864 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataaattgacggggggccc 923

Query: 901 gcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggctctt 960
|||||

Sbjct: 924 gcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggcctt 983

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
|||||

Sbjct: 984 gacatccacggaattctgcagagatgcggaagtgcccttcgggaacctgagacaggtgct 1043

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1080
|||||

Sbjct: 1044 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1103

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
|||||

Sbjct: 1104 ccttatcctttgttgccagcgattcggtcgggaactcaaaggagactgccggtgataaac 1163

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccaggggtacacacgt 1200
|||||

Sbjct: 1164 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccaggggtacacacgt 1223

Query: 1201 gctacaatggcgcatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
|||||

Sbjct: 1224 gctacaatggcgcatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1283

Query: 1261 cgtcgtagtagcggttggagtctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
|||||

Sbjct: 1284 cgtcgtagtagcggttggagtctgcaactcgactccgtgaagtcggaatcgctagtaatc 1343

Query: 1321 gtggatcagaatgccacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
|||||

Sbjct: 1344 gtagatcagaatgctacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1403

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440

|||||
Sbjct: 1404 atgggagtggttgcaaaagaagtaggtagcttaa-cttcgggagggcgcttaccacttt 1462

Query: 1441 gtgattcat 1449

|||||
Sbjct: 1463 gtgattcat 1471

>gi|4753688|emb|AJ010485.1|EAM010485 Erwinia amylovora 16S rRNA gene, tRNA-Glu g
gene
Length = 2016

Score = 2444 bits (1233), Expect = 0.0
Identities = 1398/1449 (96%), Gaps = 3/1449 (0%)
Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
|||||
Sbjct: 26 acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctt 83

Query: 61 tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
|
Sbjct: 84 gggtagcagagtggcggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 143

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
|||||
Sbjct: 144 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 203

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
|||||
Sbjct: 204 gcctcacaccatcggatgtgcccagatgggattagctagtaggtggggtaacggctcacc 263

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
|||||
Sbjct: 264 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 323

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
|||||
Sbjct: 324 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 383

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
|||||
Sbjct: 384 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 443

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccgggctaact 480
|| |
Sbjct: 444 ggggaagaggttaataaccttttccattgacgttaccgcgagaagaagcaccgggctaact 503

Query: 481 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540

Sbjct: 504 |||||ccgtgccagcagccgcggtaatacggagggtgcaagcggttaatcggaattactgggcgta 563

Query: 541 aagcgcacgcagcggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct: 564 aagcgcacgcagcggtctgtcaagtcggatgtgaaatccccgggcttaacctgggaact 623

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcggt 660
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Sbjct: 624 gcattcgaaactggcaggctagagtctcgtagaggggggtagaattccaggtgtagcggt 683

Query: 661 gaaatgcgtagagatctggaggaataccggtggcgaaggcgccccctggacgaagactg 720
|||||

Sbjct: 684 gaaatgcgtagagatctggaggaataccggtggcgaaggcgccccctggacgaagactg 743

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
|||||

Sbjct: 744 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 803

Query: 781 taaacgatgtcgacttggaggttggtgcccttgaggcgtggcttccggagctaacgcgtta 840
|||||

Sbjct: 804 taaacgatgtcgacttggaggttggtcccctgaggagtggcttccggagctaacgcgtta 863

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 900
|||||

Sbjct: 864 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 923

Query: 901 gcacaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggcctt 960
|||||

Sbjct: 924 gcacaagcggtaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggcctt 983

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
|||||

Sbjct: 984 gacatccacggaattctgcagagatgcggaagtgcccttcgggaacctgagacaggtgct 1043

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1080
|||||

Sbjct: 1044 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1103

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
|||||

Sbjct: 1104 ccttatcctttgttgccagcgattcggtcgggaactcaaaggagactgccggtgataaac 1163

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccagggtacacacgt 1200
|||||

Sbjct: 1164 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccagggtacacacgt 1223

Query: 1201 gctacaatggcgcatacaaagagaagcgacctcgcgagagcaagcggaacctcataaagtg 1260

```

|||||
Sbjct: 1224 gctacaatggcgcatatacaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1283

Query: 1261 cgtcgtagtcgggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
|||||
Sbjct: 1284 cgtcgtagtcgggatcgagctctgcaactcgactccgtgaagtcggaatcgctagtaatc 1343

Query: 1321 gtggatcagaatgccacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
|||
Sbjct: 1344 gtagatcagaatgctacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1403

Query: 1381 atgggagtggggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
|||||
Sbjct: 1404 atgggagtggggttgcaaaagaagtaggtagcttaa-cttcgggagggcgcttaccacttt 1462

Query: 1441 gtgattcat 1449
|||||
Sbjct: 1463 gtgattcat 1471

```

>gi|22947742|gb|AY133084.1| Uncultured gamma proteobacterium clone ccs1m2118 16S
 gene, partial sequence
 Length = 1450

Score = 2440 bits (1231), Expect = 0.0
 Identities = 1381/1430 (96%), Gaps = 1/1430 (0%)
 Strand = Plus / Plus

```

Query: 19 acacatgcaagtcgaacggtaacagggagcagcttgctgctctgctgacgagtgggcggac 78
|||||
Sbjct: 15 acacatgcaagtcgaacggtaacaggaagcagcttgctgctttgctgacgagtgggcggac 74

Query: 79 ggggtgagtaatgtctgggaaactgcctgatggaggggggataactactggaaacggtagct 138
|||||
Sbjct: 75 ggggtgagtaatgtctgggaaactgcctggtggaggggggataactactggaaacggtagct 134

Query: 139 aataccgcataacgtctacggaccaaagtgggggaccttcgggcctcatgccatcagatg 198
|||||
Sbjct: 135 aataccgcataacgtcgcaagaccaaagaggggggaccttcgggcctcttgccatcggatg 194

Query: 199 tgcccagatgggattagctagtaggtggggtaacgggtcacctaggcgacgatccctagc 258
|||||
Sbjct: 195 tgcccagatgggattagctagtaggtggggtaacgggtcacctaggcgacgatccctagc 254

Query: 259 tggctctgagaggatgaccagccacactggaactgagacacgggtccagactcctacgggag 318
|||||
Sbjct: 255 tggctctgagaggatgaccagccacactggaactgagacacgggtccagactcctacgggag 314

Query: 319 gcagcagtggggaatattgcacaatgggcgcaagcctgatgcagccatgccgcgtgtatg 378

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Sbjct: 315 |||||gcagcagtgagggaatatgacacaatgggcgcaagcctgatgcagccatgccgcgtgatg 374

Query: 379 aagaaggccttcgggttgtaaagtactttcagcggggaggaagggtgtgtggttaataac 438
|||||

Sbjct: 375 aagaagncttcgggttgtaaagtactttcagcggggaggaaggcgataagggttaataac 434
|||||

Query: 439 cgcagcaattgacgttacccgcagaagaagcaccggctaactccgtgccagcagccgcgg 498
|

Sbjct: 435 cttgtcgattgacgttacccgcagaagaagcaccggctaactccgtgccagcagccgcgg 494
|

Query: 499 taatacggaggggtgcaagcgttaatcggaattactgggcgtaaagcgcacgcaggcggtt 558
|||||

Sbjct: 495 taatacggaggggtgcaagcgttaatcggaattactgggcgtaaagcgcacgcaggcggtc 554
|||||

Query: 559 gattaagtcagatgtgaaatccccgggctcaacctgggaactgcatttgaaactggtcag 618
|

Sbjct: 555 tgtcaagtcggatgtgaaatccccgggctcaacctgggaactgcattcgaaactggcagg 614
|

Query: 619 cttgagtctcgtagagggggtagaattccaggtgtagcggtgaaatgcgtagagatctg 678
||

Sbjct: 615 ctagagtctttagagggggtagaattccaggtgtagcggtgaaatgcgtagagatctg 674
||

Query: 679 gaggaataccggtggcgaaggcgccccctggacgaagactgacgctcaggtgcgaaagc 738
|||||

Sbjct: 675 gaggaataccggtggcgaaggcgccccctggacaaagactgacgctcaggtgcgaaagc 734
|||||

Query: 739 gtggggagcaaacaggattagataaccctggtagtcacgcgctaaacgatgtcgacttgg 798
|||||

Sbjct: 735 gtggggagcaaacaggattagataaccctggtagtcacgcgctaaacgatgtcgacttgg 794
|||||

Query: 799 aggttgtgcccttgaggcgtggcttccggagctaacgcgttaagtcgaccgcctggggag 858
|||||

Sbjct: 795 aggttgtgcccttgaggcgtggcttccggagctaacgcgttaagtcgaccgcctggggag 854
|||||

Query: 859 tacggccgcaaggttaaaactcaaatgaattgacggggggcccgacaaagcgggtggagcat 918
|||||

Sbjct: 855 tacggccgcaaggttaaaactcaaatgaattgacggggggcccgacaaagcgggtggagcat 914
|||||

Query: 919 gtggtttaattcgatgcaacgcgaagaaccttacctggctcttgacatccagagaatcctg 978
|||||

Sbjct: 915 gtggtttaattcgatgcaacgcgaagaaccttacctactcttgacatccagagaacttag 974
|||||

Query: 979 cagagatgcgggagtgcccttcgggaactctgagacagggtgctgcatggctgtcgtcagct 1038
|||||

Sbjct: 975 cagagatgcttgggtgccttcgggaactctgagacagggtgctgcatggctgtcgtcagct 1034
|||||

Query: 1039 cgtgttggtgaaatgttgggttaagtcccgcaacgagcgcaacccttatccttggttgcca 1098

```

      |||
Sbjct: 1035 cgtgttggtgaaatgttggttaagtcccgcaacgagcgcaacccatatacctttgttgcca 1094
      |||

Query: 1099 gcggttcggccgggaactcaaaggagactgccggtgataaaccggaggaaggtggggatg 1158
      |||
Sbjct: 1095 gcggttaggccgggaactcaaaggagactgccagtataaactggaggaaggtggggatg 1154
      |||

Query: 1159 acgtcaagtcacatcatggcccttacgaccagggtacacacgtgctacaatggcgcataca 1218
      |||
Sbjct: 1155 acgtcaagtcacatcatggcccttacgagtaggggtacacacgtgctacaatggcgcataca 1214
      |||

Query: 1219 aagagaagcgacctcgcgagagcaagcggacctcataaagtgcgtcgtagtccggattgg 1278
      |||
Sbjct: 1215 aagagaagcgacctcgcgagagcaagcggacctcataaagtgcgtcgtagtccggattgg 1274
      |||

Query: 1279 agtctgcaactcgactccatgaagtgcgaatcgctagtaatcgtaggattcagaatgccacg 1338
      |||
Sbjct: 1275 agtctgcaactcgactccatgaagtgcgaatcgctagtaatcgtaggattcagaatgccacg 1334
      |||

Query: 1339 gtgaatacgttcccgggccttgtagacacaccgcccgtcacaccatgggagtggggttgcaaa 1398
      |||
Sbjct: 1335 gtgaatacgttcccgggccttgtagacacaccgcccgtcacaccatgggagtggggttgcaaa 1394
      |||

Query: 1399 agaagtaggtagcttaaccttcgggagggcgcttaccactttgtgattca 1448
      |||
Sbjct: 1395 agaagtaggtagcttaaccttcgggagggcgcttaccac-ttgtagattca 1443
      |||

```

>gi|4582061|emb|AJ233414.1|EMA233414 Erwinia mallotivora 16S rRNA gene (strain D)
Length = 1504

Score = 2436 bits (1229), Expect = 0.0
Identities = 1394/1449 (96%)
Strand = Plus / Plus

```

Query: 1      acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
      |||
Sbjct: 14     acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagggagcttgctcct 73
      |||

Query: 61     tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
      |||
Sbjct: 74     gggtagcagagtggcggacgggtgagtaatgtctgggaaactgcccgatggagggggataa 133
      |||

Query: 121    ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
      |||
Sbjct: 134    ctactggaaacggtagctaataaccgcataacgtcttcggaccaaagtgggggaccttcgg 193
      |||

Query: 181    gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 240
      |||

```

Sbjct: 194 gcctcacaccatcggtatgtcccagatgggattagctggttggtgaggtaacggctcacc 253

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
|||||

Sbjct: 254 aaggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 313

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
|||||

Sbjct: 314 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 373

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
|||||

Sbjct: 374 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 433

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
|||||

Sbjct: 434 ggtggtggggttaataaccttatcaattgacgttaccgcgagaagaagcaccggctaact 493

Query: 481 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 540
|||||

Sbjct: 494 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 553

Query: 541 aagcgacgcagggcggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
|||||

Sbjct: 554 aagcgacgcagggcggtctgttaagtcagatgtgaaatccccgggcttaacctgggaact 613

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcggt 660
|||||

Sbjct: 614 gcatttgaaactggcaggcttgagtctcgtagaggggggtagaattccaggtgtagcggt 673

Query: 661 gaaatgcgtagagatctggaggaataccggtggcgaggcgccccctggacgaagactg 720
|||||

Sbjct: 674 gaaatgcgtagagatctggaggaataccggtggcgaggcgccccctggacaaagactg 733

Query: 721 acgctcaggtgcgaaagcggtggggagcaaacaggattagataccctggtagtccacgccg 780
|||||

Sbjct: 734 acgctcaggtgcgaaagcggtggggagcaaacaggattagataccctggtagtccacgccg 793

Query: 781 taaacgatgtcgacttgagggttggtgcccttgaggcggtggttccggagctaacgcgtta 840
|||||

Sbjct: 794 taaacgatgtcgatttgagggttggtgcccttgaggcggtggttccgtagctaacgcgtta 853

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 900
|

Sbjct: 854 aatcgaccgcctggggagtagcgccgcaagggttaaaactcaaatagaattgacggggggccc 913

Query: 901 gcacaagcggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctgggtctt 960
|||||

```
Query: 1      acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
              |||
Sbjct: 4      acgctggcggcaggcctaacacatgcaagtcgaacggtagcacagag-agcttgct-ctc 61
```


4/22/03

Query: 781 taaacgatgtcgacttggaggttggtcccttgaggcggtggttccggagctaacgcgtta 840
|||||
Sbjct: 782 taaacgatgtcgacttggaggttggtcccttgaggagtggttccggagctaacgcgtta 841

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataaattgacggggggccc 900
|||||
Sbjct: 842 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataaattgacggggggccc 901

Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
|||||
Sbjct: 902 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 961

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcttccgggaactctgagacaggtgct 1020
|||||
Sbjct: 962 gacatccagagaacttagcagagatgcttgggtgccttccgggaactctgagacaggtgct 1021

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1080
|||||
Sbjct: 1022 gcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgcaac 1081

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
|||||
Sbjct: 1082 ccttatcctttgttgccagcgattcggycggaactcaaaggagactgccagtgataaac 1141

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
|||||
Sbjct: 1142 tggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacacgt 1201

Query: 1201 gctacaatggcgcatatacaagagaagcgacctcgcgagagcaagcggacctcataaagt 1260
|||||
Sbjct: 1202 gctacaatggcgcatatacaagagaagcgacctcgcgagagcaagcggacctcataaagta 1261

Query: 1261 cgtcgtagtcgggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
|||||
Sbjct: 1262 tgtcgtagtcgggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1321

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
|||||
Sbjct: 1322 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1381

Query: 1381 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
|||||
Sbjct: 1382 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1441

Query: 1441 gtgattcat 1449
|||||
Sbjct: 1442 gtgattcat 1450

Score = 2432 bits (1227), Expect = 0.0
Identities = 1392/1449 (96%), Gaps = 2/1449 (0%)
Strand = Plus / Plus

| | | |
|------------|--|-----|
| Query: 1 | acgctggcggcaggcctaacacatgcaagtcgaacggtaaacagggagcagcttgctgctc | 60 |
| | | |
| Sbjct: 6 | acgctggcggcaggcctaacacatgcaagtcgarcggtarcacagag-agcttgct-ctc | 63 |
| | | |
| Query: 61 | tgctgacgagtgccggacgggtgagtaaatgtctgggaaactgcctgatggagggggataa | 120 |
| | | |
| Sbjct: 64 | gggtgacgagygccggacgggtgagtaaatgtctgggaaactgcctgatggagggggataa | 123 |
| | | |
| Query: 121 | ctactggaaacggtagctaataaccgcataacgtctacggaccaaaagtgggggaccttcgg | 180 |
| | | |
| Sbjct: 124 | ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaaagagggggaccttcgg | 183 |
| | | |
| Query: 181 | gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc | 240 |
| | | |
| Sbjct: 184 | gcctcttgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc | 243 |
| | | |
| Query: 241 | taggcgacgatccctagctgggtctgagaggatgaccagccacactggaactgagacacgg | 300 |
| | | |
| Sbjct: 244 | taggcgacgatccctagctgggtctgagaggatgaccagccacactggaactgagacacgg | 303 |
| | | |
| Query: 301 | tccagactcctacgggagggcagcagtggggaatattgcacaatgggcgcaagcctgatgc | 360 |
| | | |
| Sbjct: 304 | tccagactcctacgggagggcagcagtggggaatattgcacaatgggcgcaascctgatgc | 363 |
| | | |
| Query: 361 | agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtaactttcagcggggaggaa | 420 |
| | | |
| Sbjct: 364 | agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtaactttcagcggggaggaa | 423 |
| | | |
| Query: 421 | gggtgttggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact | 480 |
| | | |
| Sbjct: 424 | ggcgataaggttaataaccttgctgattgacgttaccgcgagaaraagcaccggctaact | 483 |
| | | |
| Query: 481 | ccgtgccagcagccgcggtaatacggaggggtgcaagcggttaatcggaattactgggcgta | 540 |
| | | |
| Sbjct: 484 | ccgtgccagcagccgcggtaatacggaggggtgcaagcggttaatcggaattactgggcgta | 543 |
| | | |
| Query: 541 | aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact | 600 |
| | | |
| Sbjct: 544 | aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact | 603 |

[illegible]

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Query: 1141 cggaggaaggtggggatgacgtcaagtcacatcatggcccttacgaccagggctacacacgt 1200
 |||||
 Sbjct: 1144 tggaggaaggtggggatgacgtcaagtcacatcatggcccttacgagtagggctacacacgt 1203

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagt 1260
 |||||
 Sbjct: 1204 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1263

Query: 1261 cgtcgtagtcggttgaggctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
 |||||
 Sbjct: 1264 tgtcgtagtcggttgaggctctgcaactcgactccatgaagtcggaatcgctagtaatc 1323

Query: 1321 gtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
 |||||
 Sbjct: 1324 gtagatcagaatgctacggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1383

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
 |||||
 Sbjct: 1384 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1443

Query: 1441 gtgattcat 1449
 |||||
 Sbjct: 1444 gtgattcat 1452

>gi|22758992|gb|AF534213.1| Uncultured bacterium clone Phe50 16S ribosomal RNA g
 sequence
 Length = 1462

Score = 2428 bits (1225), Expect = 0.0
 Identities = 1395/1449 (96%), Gaps = 2/1449 (0%)
 Strand = Plus / Minus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
 |||||
 Sbjct: 1457 acgctggcggcaggcctaacacatgcaagtcgagcggtaacacagag-agcttgct-ctc 1400

Query: 61 tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
 |||||
 Sbjct: 1399 gggtagcagcggcgacgggtgagtaatgtctgggaaactgcctgatggagggggataa 1340

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
 |||||
 Sbjct: 1339 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgg 1280

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 240
 |||||
 Sbjct: 1279 gcctcttgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 1220

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
|||||
Sbjct: 1219 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 1160

Query: 301 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
|||||
Sbjct: 1159 tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 1100

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
|||||
Sbjct: 1099 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 1040

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
|||
Sbjct: 1039 ggcgataagggttaataaccttgctcgattgacgttaccgcgaggaagaagcaccggctaact 980

Query: 481 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 540
|||||
Sbjct: 979 ccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcgta 920

Query: 541 aagcgcacgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaact 600
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Sbjct: 919 aagcgcacgcaggcgggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaact 860

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccaggtgtagcgg 660
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Sbjct: 859 gcattcgaaactggcaggctagagtcttgtagaggggggtagaattccaggtgtagcgg 800

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcggccccctggacgaagactg 720
|||||
Sbjct: 799 gaaatgcgtagagatctggaggaataaccggtggcgaaggcggccccctggacaaagactg 740

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
|||||
Sbjct: 739 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 680

Query: 781 taaacgatgtcgacttggaggttggtgcccttgaggcggtggcttccggagctaacgcgtta 840
|||||
Sbjct: 679 taaacgatgtcgacttggaggttggtgcccttgaggcggtggcttccggagctaacgcgtta 620

Query: 841 agtcgaccgcctggggagtagcggccgcaagggttaaaactcaaataaattgacggggggccc 900
|||||
Sbjct: 619 agtcgaccgcctggggagtagcggccgcaagggttaaaactcaaataaattgacggggggccc 560

Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
|||||
Sbjct: 559 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 500

Query: 961 gacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtgct 1020
 |||||
 Sbjct: 499 gacatccagagaacttagcagagatgctttggtgccttcgggaactctgagacaggtgct 440

Query: 1021 gcatggctgtcgtcagctcgtgttgtaaagtgggttaagtcgcaacgagcgcaac 1080
 |||||
 Sbjct: 439 gcatggctgtcgtcagctcgtgttgtaaagtgggttaagtcgcaacgagcgcaac 380

Query: 1081 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
 |||||
 Sbjct: 379 ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccagtgataaac 320

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
 |||||
 Sbjct: 319 tggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacacgt 260

Query: 1201 gctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
 |||||
 Sbjct: 259 gctacaatggcgcatataaaagagaagcggaactcgcgagagcaagcggacctcataaagtg 200

Query: 1261 cgtcgtagtcgggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
 |||||
 Sbjct: 199 cgtcgtagtcgggattggagctctgcaactcgactccatgaagtcggaatcgctagtaatc 140

Query: 1321 gtggatcagaatgccacggtgaatacggtcccgggccttgtagacacaccgcccgtcacacc 1380
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 Sbjct: 139 gtagatcagaatgctacggtgaatacggtcccgggccttgtagacacaccgcccgtcacacc 80

Query: 1381 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
 |||||
 Sbjct: 79 atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 20

Query: 1441 gtgattcat 1449
 |||||
 Sbjct: 19 gtgattcat 11

>gi|4581975|emb|AJ233405.1|BNO233405 Buttiauxella noackiae 16S rRNA gene (strain
 Length = 1497

Score = 2422 bits (1222), Expect = 0.0
 Identities = 1396/1451 (96%), Gaps = 6/1451 (0%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggta--acagggagcagcttgctgc 58
 |||||
 Sbjct: 12 acgctggcggcaggcctaacacatgcaagtcgagcggtagcacagggagc---ttgctcc 68

Query: 59 tctgctgacgagtgccggacgggtgagtaatgtctgggaaactgcctgatggagggggat 118

4/22/03

```
|||||
Sbjct: 788 cgtaaacgatgtcgacttggaggttgttcccttgaggagtggcttccggagctaacgcgt 847

Query: 839 taagtcgaccgcctggggagtacggccgcaagggttaaaactcaaataaattgacgggggc 898
|||||
Sbjct: 848 taagtcgaccgcctggggagtacggccgcaagggttaaaactcaaataaattgacgggggc 907

Query: 899 ccgcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtc 958
|||||
Sbjct: 908 ccgcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactc 967

Query: 959 ttgacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtg 1018
|||||
Sbjct: 968 ttgacatccacggaattcggcagagatgccttagtgcccttcgggaaccgtgagacaggtg 1027

Query: 1019 ctgcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgca 1078
|||||
Sbjct: 1028 ctgcatggctgtcgtcagctcgtgttgtaaattggtgggttaagtcccgcaacgagcgca 1087

Query: 1079 acccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataa 1138
|||||
Sbjct: 1088 acccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccagtgataa 1147

Query: 1139 accggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacac 1198
|||||
Sbjct: 1148 actggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacac 1207

Query: 1199 gtgctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaag 1258
|||||
Sbjct: 1208 gtgctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaag 1267

Query: 1259 tgcgtcgtagtcgggattggagtcgcaactcgactccatgaagtcggaatcgctagtaa 1318
|||||
Sbjct: 1268 tgcgtcgtagtcgggattggagtcgcaactcgactccgtgaagtcggaatcgctagtaa 1327

Query: 1319 tcgtggatcagaatgccacggtgaatacgttccccgggccttgtagacacaccgcccgtcaca 1378
|||||
Sbjct: 1328 tcgtagatcagaatgctacggtgaatacgttccccgggccttgtagacacaccgcccgtcaca 1387

Query: 1379 ccatgggagtggttgcaaaaagaagtaggttagcttaaccttcgggagggcgcttaccact 1438
|||||
Sbjct: 1388 ccatgggagtggttgcaaaaagaagtaggttagcttaaccttcgggagggcgcttaccact 1447

Query: 1439 ttgtgattcat 1449
|||||
Sbjct: 1448 ttgtgattcat 1458
```

>gi|18419669|gb|AF463533.1| Citrobacter sp. TSA-1 16S ribosomal RNA gene, partial
Length = 1456

Score = 2420 bits (1221), Expect = 0.0

Identities = 1386/1441 (96%)

Strand = Plus / Plus

```
Query: 9      ggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctctgctgacg 68
             |||
Sbjct: 1      ggcaggcctaacacatgcaagtcgaacggtagcacagaggagcttgctccttgggtgacg 60

Query: 69     agtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataactactgga 128
             |||
Sbjct: 61     agtggcggacgggtgagtaatgtctgggaaactgcccgatggagggggataactactgga 120

Query: 129    aacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgggcctcatg 188
             |||
Sbjct: 121    aacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgggcctcttg 180

Query: 189    ccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacctaggcgac 248
             |||
Sbjct: 181    ccatcggatgtgcccagatgggattagctagtaggtggggtaacgggtcacctaggcgac 240

Query: 249    gatccctagctggtctgagaggatgaccagccacactggaactgagacacgggtccagact 308
             |||
Sbjct: 241    gatccctagctggtctgagaggatgaccagccacactggaactgagacacgggtccagact 300

Query: 309    cctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgcagccatgc 368
             |||
Sbjct: 301    cctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgcagccatgc 360

Query: 369    cgcggtgatgaagaaggccttcggggtgtaaagtactttcagcggggaggaagggtgttgt 428
             |||
Sbjct: 361    cgcggtgatgaagaaggccttcggggtgtaaagtactttcagcggaggaggaaggcattgt 420

Query: 429    ggttaataaccgcagcaattgacgttaccgcagaagaagcaccgggctaactccgtgcca 488
             |||
Sbjct: 421    ggttaataaccgcagtgattgacgttactcgcagaagaagcaccgggctaactccgtgcca 480

Query: 489    gcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgtaaagcgcac 548
             |||
Sbjct: 481    gcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgtaaagcgcac 540

Query: 549    gcaggcggttgattaagtcagatgtgaaatccccgggctcaacctgggaactgcatttga 608
             |||
Sbjct: 541    gcaggcggtctgtcaagtcggatgtgaaatccccgggctcaacctgggaactgcattccga 600

Query: 609    aactggtcagcttgagtctcgtagaggggggtagaattccagggtgtagcggtgaaatgcg 668
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```

Sbjct: 601 aactggcaggctagagtcttgtagaggggggtagaattccagggtgtagcggtgaaatgcg 660

Query: 669 tagagatctggaggaataccggtggcgaaggcggccccctggacgaagactgacgctcag 728
|||||

Sbjct: 661 tagagatctggaggaataccggtggcgaaggcggccccctggacaaagactgacgctcag 720

Query: 729 gtgcgaaagcgtggggagcaaacaggattagataaccctggtagtccacgccgtaaacgat 788
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Sbjct: 721 gtgcgaaagcgtggggagcaaacaggattagataaccctggtagtccacgccgtaaacgat 780

Query: 789 gtcgacttgagggttggtgcccttgaggcgtggcttccggagctaacgcgttaagtgcgacc 848
|||||

Sbjct: 781 gtcgacttgagggttggtgcccttgaggcgtggcttccggagctaacgcgttaagtgcgacc 840

Query: 849 gcctggggagtagcggccgcaagggttaaaactcaaatgaattgacggggggcccgcacaaagc 908
|||||

Sbjct: 841 gcctggggagtagcggccgcaagggttaaaactcaaatgaattgacggggggcccgcacaaagc 900

Query: 909 ggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctgggtcttgacatcca 968
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Sbjct: 901 ggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactcttgacatcca 960

Query: 969 gagaatcctgcagagatgcgggagtgcccttcgggaactctgagacagggtgctgcatggct 1028
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Sbjct: 961 gagaacttagcagagatgctttggtgccttcgggaactctgagacagggtgctgcatggct 1020

Query: 1029 gtcgtcagctcgtgttgtaaatgttgggttaagtcccgcaacgagcgcaacccttatcc 1088
|||||

Sbjct: 1021 gtcgtcagctcgtgttgtaaatgttgggttaagtcccgcaacgagcgcaacccttatcc 1080

Query: 1089 tttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataaaccggaggaa 1148
|||||

Sbjct: 1081 tttgttgccagcgggttcggccgggaactcaaaggagactgccagtataaactggaggaa 1140

Query: 1149 ggtgggggatgacgtcaagtcacatcatggcccttacgaccagggtacacacgtgctacaat 1208
|||||

Sbjct: 1141 ggtgggggatgacgtcaagtcacatcatggcccttacgagtaggggtacacacgtgctacaat 1200

Query: 1209 ggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtgcgtcgtag 1268
|||

Sbjct: 1201 ggcatataaaagagaagcgacctcgcgagagcaagcggacctcataaagtatgctcgtag 1260

Query: 1269 tccggattggagctctgcaactcgactccatgaaatcggaatcgctagtaatcgtaggatca 1328
|||||

Sbjct: 1261 tccggattggagctctgcaactcgactccatgaaatcggaatcgctagtaatcgtaggatca 1320

Query: 1329 gaatgccacgggtgaatacgttccccgggccttgtagacacaccgcccgtcacaccatggggagt 1388
|||||

Sbjct: 1321 gaatgccacggtgaatacgttccccgggccttgtaacacacgcccgtcacaccatgggagtg 1380

Query: 1389 ggggttgcaaaagaagtaggttagcttaaccttcgggagggcgcttaccactttgtgattca 1448
 |||||

Sbjct: 1381 ggggttgcaaaagaagtaggttagcttaaccttcgggagggcgcttaccactttgtgattca 1440

Query: 1449 t 1449

|
 Sbjct: 1441 t 1441

>gi|3282037|emb|Y17663.1|KPY17663 Klebsiella planticola 16S rRNA gene, strain 74
 Length = 1452

Score = 2420 bits (1221), Expect = 0.0
 Identities = 1392/1449 (96%), Gaps = 2/1449 (0%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
 |||||
 Sbjct: 4 acgctggcggcaggcctaacacatgcaagtcgagcggtagcacagag-agcttgct-ctc 61

Query: 61 tgctgacgagtgggcgacgggtgagtaatgtctgggaaactgcctgatggaggggggataa 120
 | |||||
 Sbjct: 62 gggtgacgagcgggcgacgggtgagtaatgtctgggaaactgcctgatggaggggggataa 121

Query: 121 ctactggaaacggtagctaataccgcataacgtctacggaccaaagtgggggaccttcgg 180
 |||||
 Sbjct: 122 ctactggaaacggtagctaataccgcataacgtcgcaagaccaaagtgggggaccttcgg 181

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacc 240
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 Sbjct: 182 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaaatggctcacc 241

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
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Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccgggctaact 480
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 Strand = Plus / Plus

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 Sbjct: 1382 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1441

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 Sbjct: 1442 gtgattcat 1450

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 CF01Ent-1
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 Strand = Plus / Plus

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Sbjct: 493 ctccgtgccagcagccgcggttaatacggaggggtgcaagcggttaatcggaattactgggcg 552

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Length = 1441

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Strand = Plus / Plus

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 Strand = Plus / Plus

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 Sbjct: 62 gaaacggtagctaataaccgcataacgtcgcaagaccaaagagggggaccttcgggcctct 121

Query: 187 tgccatcagatgtgcccagatgggattagctagtaggtggggtaacggctcacctaggcg 246
 |||||
 Sbjct: 122 tgccatcagatgtgcccagatgggattagctagtagtggtggggtaacggctcacctaggcg 181

Query: 247 acgatccctagctggtctgagaggatgaccagccacactggaactgagacacgggtccaga 306
 |||||
 Sbjct: 182 acgatccctagctggtctgagaggatgaccagccacactggaactgagacacgggtccaga 241

Query: 307 ctccctacgggagggcagcagtggggaatattgcacaatgggcgcaagcctgatgcagccat 366
 |||||
 Sbjct: 242 ctccctacgggagggcagcagtggggaatattgcacaatgggcgcaagcctgatgcagccat 301

Query: 367 gccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaagggtgtt 426
 |||||
 Sbjct: 302 gccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaagggtgtt 361

Query: 427 gtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaactccgtgc 486
 |||||
 Sbjct: 362 gaggttaataacctcagcaattgacgttaccgcgagaagaagcaccggctaactccgtgc 421

Query: 487 cagcagccgcggtaataaccgaggggtgcaagcggttaatcggaattactgggcgtaaagcgc 546
 |||||
 Sbjct: 422 cagcagccgcggtaataaccgaggggtgcaagcggttaatcggaattactgggcgtaaagcgc 481

Query: 547 acgcaggcgggttgattaagtcagatgtgaaatccccgggctcaacctgggaactgcattt 606

4/22/03


```

      |||
Sbjct: 1202 agtccggattggagctgcaactcgactccatgaagtcggaatcgctagtaatcgtagat 1261

Query: 1327 cagaatgccacggtgaatacgttccccgggccttgtagacacaccgcccgtcacaccatggga 1386
      |||
Sbjct: 1262 cagaatgctacggtgaatacgttccccgggccttgtagacacaccgcccgtcacaccatggga 1321

Query: 1387 gtgggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccactttgtgatt 1446
      |||
Sbjct: 1322 gtgggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccactttgtgatt 1381

Query: 1447 cat 1449
      |||
Sbjct: 1382 cat 1384

```

>gi|3282054|emb|Y17669.1|KPY17669 Klebsiella pneumoniae 16S rRNA gene, strain K1
Length = 1452

Score = 2416 bits (1219), Expect = 0.0
Identities = 1391/1449 (95%), Gaps = 2/1449 (0%)
Strand = Plus / Plus

```

Query: 1      acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
      |||
Sbjct: 4      acgctggcggcaggcctaacacatgcaagtcgagcggtagcacagag-agcttgct-ctc 61

Query: 61     tgctgacgagtggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
      |||
Sbjct: 62     gggtgacgagcggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 121

Query: 121    ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
      |||
Sbjct: 122    ctactggaaacggtagctaataaccgcataaygtcgcaagaccaaagtgggggaccttcgg 181

Query: 181    gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 240
      |||
Sbjct: 182    gcctcatgccatcagatgtgccagatgggattagctagtaggtggggtaacggctcacc 241

Query: 241    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
      |||
Sbjct: 242    taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 301

Query: 301    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 360
      |||
Sbjct: 302    tccagactcctacgggaggcagcagtggggaatattgcacaatgggcgcaagcctgatgc 361

Query: 361    agccatgccgcgtgtatgaagaaggccttcggggtgtaaagtactttcagcggggaggaa 420
      |||

```

4/22/03

Sbjct: 1082 ccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccagtgataaac 1141

Query: 1141 cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
 |||

Sbjct: 1142 tggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1201

Query: 1201 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagtg 1260
 |||

Sbjct: 1202 gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1261

Query: 1261 cgtcgtagtcgggattggagtcctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
 |||

Sbjct: 1262 tgtcgtagtcgggattggagtcctgcaactcgactccatgaagtcggaatcgctagtaatc 1321

Query: 1321 gtggatcagaatgccacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1380
 |||

Sbjct: 1322 gtagatcagaatgctacgggtgaatacgttcccgggccttgtagacacaccgcccgtcacacc 1381

Query: 1381 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
 |||

Sbjct: 1382 atgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1441

Query: 1441 gtgattcat 1449
 |||

Sbjct: 1442 gtgattcat 1450

>gi|6562390|emb|AJ251468.1|EAE251468 Enterobacter aerogenes partial 16S rRNA gen
 Length = 1511

Score = 2416 bits (1219), Expect = 0.0
 Identities = 1392/1449 (96%), Gaps = 2/1449 (0%)
 Strand = Plus / Plus

Query: 1 acgctggcggcaggcctaacacatgcaagtcgaacggtaacagggagcagcttgctgctc 60
 |||
 Sbjct: 4 acgctggcggcaggcctaacacatgcaagtcgagcggtaacacagag-agcttgct-ctc 61

Query: 61 tgctgacgagtgccggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 120
 |||
 Sbjct: 62 gggtagcagcggcggacgggtgagtaatgtctgggaaactgcctgatggagggggataa 121

Query: 121 ctactggaaacggtagctaataaccgcataacgtctacggaccaaagtgggggaccttcgg 180
 |||
 Sbjct: 122 ctactggaaacggtagctaataaccgcataacgtcgcaagaccaaagtgggggaccttcgg 181

Query: 181 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 240
 |||
 Sbjct: 182 gcctcatgccatcagatgtgcccagatgggattagctagtaggtggggtaacgggtcacc 241

Query: 241 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 300
|||
Sbjct: 242 taggcgacgatccctagctggtctgagaggatgaccagccacactggaactgagacacgg 301

Query: 301 tccagactcctacgggaggcagcagtgagggaatattgcacaatgggcgcaagcctgatgc 360
|||
Sbjct: 302 tccagactcctacgggaggcagcagtgagggaatattgcacaatgggcgcaagcctgatgc 361

Query: 361 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 420
|||
Sbjct: 362 agccatgccgcgtgtatgaagaaggccttcgggttgtaaagtactttcagcggggaggaa 421

Query: 421 ggtgttggtggttaataaccgcagcaattgacgttaccgcgagaagaagcaccggctaact 480
|||
Sbjct: 422 ggcgttaaggttaataaaccttggcgattgacgttactcgcaagaagaagcaccggctaact 481

Query: 481 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 540
|||
Sbjct: 482 ccgtgccagcagccgcggttaatacggagggtgcaagcggttaatcggaattactgggcgta 541

Query: 541 aagcgcacgcaggcggttgattaagtacagatgtgaaatccccgggctcaacctgggaact 600
|||
Sbjct: 542 aagcgcacgcaggcggtctgtcaagtgcgatgtgaaatccccgggctcaacctgggaact 601

Query: 601 gcatttgaaactggtcagcttgagtctcgtagaggggggtagaattccagggtgtagcggt 660
|||
Sbjct: 602 gcattcgaaactggcaggctagagtcttgtagaggggggtagaattccagggtgtagcggt 661

Query: 661 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacgaagactg 720
|||
Sbjct: 662 gaaatgcgtagagatctggaggaataaccggtggcgaaggcgccccctggacaaagactg 721

Query: 721 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 780
|||
Sbjct: 722 acgctcaggtgcgaaagcgtggggagcaaacaggattagataccctggtagtccacgccg 781

Query: 781 taaacgatgtcgacttgagggttggtgcccttgaggcgtggcttccggagctaacgcgtta 840
|||
Sbjct: 782 taaacgatgtcgacttgagggttggtgcccttgaggcgtggcttccggagctaacgcgtta 841

Query: 841 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataaattgacggggggccc 900
|||
Sbjct: 842 agtcgaccgcctggggagtagcgccgcaagggttaaaactcaaataaattgacggggggccc 901

Query: 901 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtctt 960
|||
Sbjct: 902 gcacaagcgggtggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactctt 961

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Query: 961   gacatccagagaatcctgcagagatgcgggagtccttcgggaactctgagacaggtgct 1020
          |||
Sbjct: 962   gacatccagagaacttagcagagatgctttggtgccttcgggaactctgagacaggtgct 1021

Query: 1021  gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1080
          |||
Sbjct: 1022  gcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgcaac 1081

Query: 1081  ccttatcctttgttgccagcggttcggccgggaactcaaaggagactgccggtgataaac 1140
          |||
Sbjct: 1082  ccttatcctttgttgccagcgrtycggccgggaactcaaaggagactgccagtataaac 1141

Query: 1141  cggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacacgt 1200
          |||
Sbjct: 1142  tggaggaaggtggggatgacgtcaagtcacatggcccttacgagtagggctacacacgt 1201

Query: 1201  gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagt 1260
          |||
Sbjct: 1202  gctacaatggcgcatatacaaagagaagcgacctcgcgagagcaagcggacctcataaagta 1261

Query: 1261  cgtcgtagtcgggattggagtcctgcaactcgactccatgaagtcggaatcgctagtaatc 1320
          |||
Sbjct: 1262  tgtcgtagtcgggattggagtcctgcaactcgactccatgaagtcggaatcgctagtaatc 1321

Query: 1321  gtggatcagaatgccacgggtgaatacgttcccgggcttgtagacacaccgcccgtcacacc 1380
          |||
Sbjct: 1322  gtagatcagaatgctacgggtgaatacgttcccgggcttgtagacacaccgcccgtcacacc 1381

Query: 1381  atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1440
          |||
Sbjct: 1382  atgggagtggttgcaaaagaagtaggtagcttaaccttcgggagggcgcttaccacttt 1441

Query: 1441  gtgattcat 1449
          |||
Sbjct: 1442  gtgattcat 1450

```

>gi|4581974|emb|AJ233404.1|BIZ233404 Butiauxella izardii 16S rRNA gene (strain
Length = 1498

Score = 2415 bits (1218), Expect = 0.0
Identities = 1395/1451 (96%), Gaps = 6/1451 (0%)
Strand = Plus / Plus

```

Query: 1      acgctggcggcaggcctaacacatgcaagtcgaacggta--acagggagcagcttgctgc 58
          |||
Sbjct: 12     acgctggcggcaggcctaacacatgcaagtcgagcggtagcacagggagc---ttgctcc 68

```


Query: 779 cgtaaacgatgtcgacttggaggttgtgcccttgaggcgtggcttccggagctaacgcgt 838
|||
Sbjct: 788 cgtaaacgatgtcgacttggaggttgttcccttgaggagtggcttccggagctaacgcgt 847

Query: 839 taagtcgaccgcctggggagtacggccgcaagggttaaaactcaaataaattgacgggggc 898
|||
Sbjct: 848 taagtcgaccgcctggggagtacggccgcaagggttaaaactcaaataaattgacgggggc 907

Query: 899 ccgcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctggtc 958
|||
Sbjct: 908 ccgcacaagcggaggagcatgtggtttaattcgatgcaacgcgaagaaccttacctactc 967

Query: 959 ttgacatccagagaatcctgcagagatgcgggagtgcccttcgggaactctgagacaggtg 1018
|||
Sbjct: 968 ttgacatccacggaatttggcagagatgccttagtgcccttcgggaacctgagacaggtg 1027

Query: 1019 ctgcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgca 1078
|||
Sbjct: 1028 ctgcatggctgtcgtcagctcgtgttgtaaagtgtgggttaagtcccgcaacgagcgca 1087

Query: 1079 acccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccggtgataa 1138
|||
Sbjct: 1088 acccttatcctttgttgccagcgggttcggccgggaactcaaaggagactgccagtataa 1147

Query: 1139 accggaggaaggtggggatgacgtcaagtcacatggcccttacgaccagggtacacac 1198
|||
Sbjct: 1148 actggaggaaggtggggatgacgtcaagtcacatggcccttacgagtaggggtacacac 1207

Query: 1199 gtgctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaag 1258
|||
Sbjct: 1208 gtgctacaatggcgcatataaaagagaagcgacctcgcgagagcaagcggacctcataaag 1267

Query: 1259 tgcgtcgtagtcgggattggagctctgcaactcgactccatgaagtcggaatcgctagtaa 1318
|||
Sbjct: 1268 tgcgtcgtagtcgggatcgagctctgcaactcgactccgtgaagtcggaatcgctagtaa 1327

Query: 1319 tcgtggatcagaatgccacggtgaatacgttcccgggccttgtagacacaccgcccgtcaca 1378
|||
Sbjct: 1328 tcgtagatcagaatgctacggtgaatacgttcccgggccttgtagacacaccgcccgtcaca 1387

Query: 1379 ccatgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccact 1438
|||
Sbjct: 1388 ccatgggagtggttgcaaaaagaagtaggtagcttaaccttcgggagggcgcttaccact 1447

Query: 1439 ttgtgattcat 1449
|||
Sbjct: 1448 ttgtgattcat 1458

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,
or phase 0, 1 or 2 HTGS sequences)

Posted date: Apr 21, 2003 12:40 AM

Number of letters in database: -300,496,531

Number of sequences in database: 1,729,678

| Lambda | K | H |
|--------|-------|------|
| 1.37 | 0.711 | 1.31 |

Gapped

| Lambda | K | H |
|--------|-------|------|
| 1.37 | 0.711 | 1.31 |

Matrix: blastn matrix:1 -3

Gap Penalties: Existence: 5, Extension: 2

Number of Hits to DB: 4,444,676

Number of Sequences: 1729678

Number of extensions: 4444676

Number of successful extensions: 562618

Number of sequences better than 10.0: 94638

Number of HSP's better than 10.0 without gapping: 94564

Number of HSP's successfully gapped in prelim test: 74

Number of HSP's that attempted gapping in prelim test: 29112

Number of HSP's gapped (non-prelim): 463289

length of query: 1449

length of database: 8,289,438,057

effective HSP length: 22

effective length of query: 1427

effective length of database: 8,251,385,141

effective search space: 11774726596207

effective search space used: 11774726596207

T: 0

A: 0

X1: 6 (11.9 bits)

X2: 15 (29.7 bits)

S1: 12 (24.3 bits)

S2: 20 (40.1 bits)